

Sequence Listing

0110> Baker, Kevin P.
 Binstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Liang
 Giddard, Audrey
 Godowski, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.



0120> Secreted and Transmembrane Polypeptides and Nucleic
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50 55 60
Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
65 70 75
Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
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aaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
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<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171,198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

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Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
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Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val			

02100 11
 02110 2720
 02120 DNA
 02130 Homo sapiens

04000 11
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 gagctctcgg ttctctcag tcggaattcc tgaagcgcgc agtgggcggg 100
 ggccttggg ccgtcgcac cactgtagtc atgtaaccac cgcgcgcgc 150
 gaggctcat cgggaattca tctcggtagc gctgagcttt ggcgagagct 200

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 cctctcggcc gcccgcagg gggcttggag ggtcggacgg caagtccgtc 2650
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 ttgatttgc ctacccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro	35	40	45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr	50	55	60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp	65	70	75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu	80	85	90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala	95	100	105
Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile			

	290		295		300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser		
	305		310		315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu		
	320		325		330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu		
	335		340		345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn		
	350		355		360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser		
	365		370		375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr		
	380		385		390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe		
	395		400		405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala		
	410		415		420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys		
	425		430		435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe		
	440		445		450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr		
	455		460		465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu		
	470		475		480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg		
	485		490		495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val		
	500		505		510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu		
	515		520		525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly		
	530		535		540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr		
	545		550		555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu		
	560		565		570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val		

	575		580		585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro	Glu Thr		
	590		595		600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys		
	605		610		615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe		
	620		625		630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln		
	635		640		645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe		
	650		655		660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp		
	665		670		675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala		
	680		685		690
His Pro Leu Pro	Ile Trp Thr Pro Ala				
	695				

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 <111> 24
 <112> DNA
 <113> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 13
 cggcagaagg gogtgattga cgtc 24

<110> 14
 <111> 24
 <112> DNA
 <113> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 14
 ccctctttct tcccagacag gcgc 24

<110> 15
 <111> 44
 <112> DNA
 <113> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagttagtg gtttggctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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cctcggaag tgttcctct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttctctct cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cgggcagtcg ggggacaagg gcaggagacc tcgggcctc ccctgctctg 300
ccccccagag cggcccctg agcactggga agaagacgca tctggggcc 350
cccacgcctt ggcagtgctg gtgcctctcc gcgaaagctt cgaggagctc 400
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gcacacatc tacgtgctca accaggtgga ccaattcagg tccaacggg 500
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tggcttctct gaggtctggc ccttcacgtt ggctcccg gagctcacc 650
ctctctacca ctacaagac tatgtcggcg gcctcctgt gctctcacc 700
cagcactacc ggtgtgcaa tgggatgtcc aacgctctt gggctctggg 750
ccgcagggac gacgagttct accgggcct taaggagctt gggctcagc 800
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 tgaacaggac aacctctcat cccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PPT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu	150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp	165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala	180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His	195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His	210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly	225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu	240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe	255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg	270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly	285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu	300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp	315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser				330

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
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<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
ggagtggggg aagacacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
cttctctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggtcgg tgcacagaaa gtctcttctg ccactgaagc ccccatcagg 150
gatggtgcct tctttccccc ttcttttctg tgtctcctgc ctcatgggc 200
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ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
attatataaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgttttca atgtttgtaa agattgttct gtgtaaaatat gtctttataa 450

taaacagttta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> FRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2383

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg oggcccgtta ggcacgtgag ccgcgcctcg cccgcagggc 200

cccgccccc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250

cgccgtgtgt gctgcgcctc tcgtgtgttag cgtgtgtcgc gctgtgtgga 300

ggcggggggg gggcggggcg ccggcgcctg ccgcgcgggt gcaagcacga 350

tggggggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

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gaagaatggc tcattttctg gggttaagtc ccttgaaaqa ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgcctctct gggactgtca 600
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atttgtttct ttcattatct caaggaactt ttgattatct tgcgtcatta 750
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gatgggagaa tagttgaaac cgatgaatcg caaggtattt ttgttgaaaa 1100
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<213> Homo sapiens

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<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

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Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	50	55	60	
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Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	260	265	270	
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Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
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Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	
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Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
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Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	
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Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe	
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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val	
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Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr	
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				440					445					450	
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu	
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Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys	
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Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu	
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Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala	
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg	
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly	
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 575 580 585

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 <213> Homo sapiens

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 <223> Signal peptide.

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 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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(210) 31
(211) 322
(212) PFT
(213) Homo sapiens

(400) 31
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Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser	Ala Ser Ile Ile Tyr
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Pro Thr Thr Tyr	Val Gln Phe Leu Ser His	Gly Arg Ser Arg Asp
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His Ala Ile Ala	Ala Thr Phe Phe Ser Cys	Ile Ala Cys Val Ala
140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg Ala	Arg Pro Gly Glu Ile
155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly Leu	Leu Lys Val Leu Glu
170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala Phe	Ile Ser Asp Pro Asn
185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu Trp	Cys Val Ala Val Tyr
200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile Ala	Ile Leu Leu Asn Leu
215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile Pro	Phe Pro Ser Phe Leu
230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu Leu	Tyr Ala Thr Ala Leu
245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp Glu	Lys Tyr Gly Gly Gln
260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys Ser	Arg Ser His Ala Tyr
275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu Ala	Val Ala Ile Leu Thr
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<211> 3580

<212> DNA

<213> Homo sapiens

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<E11> 335

<E12> PRT

<E13> Homo sapiens

<E400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
1				5					10					15
Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgctctttgt cccagacttc tgtcc 25

<210> 35
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
ctgcatgcta atgtgtccag taaatgata ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
ttccactcaa tgaggtagc cactc 25

<210> 37
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
ggcagagccct aactatccag gag 23

<210> 38
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ctggtgcaaa gcgagctct tg 22

<210> 40
<211> 2084

<212> DNA

<213> Homo sapiens

<410> 41

ggttctgtggg cgtctgtgta cacaaggaa; atacagccag cccacctaa 50
ttttgtttcc ctggcaccct cctgatcagt ggcacattgt cacacttaac 100
ccatctgttt totctaagc agcacagatt cctttcagac aggacaaatg 150
tgatatttca gttcctgatt gtaaatcct cctcagcctg aagcttctgt 200
taactagccat tgtgagcttc agttttcttca ctgcaaaat gggcataata 250
caatctatctc ttgcacatc aagggattgt tattccttta aaaaaaac 300
aataccaaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caaagtgtgt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tcttttgaaa gtgaagcaaa cttaaacctc gataaagaaa 500
atataaccac ctcaaatctc aaggcgagtc attccctcc tttgaatctc 550
cccaacaaca gccacggcat aacagatttc tccagtaact cctcagcaga 600
gcattctttg gccagtctaa aaccacatc taccatttcc acaagccctc 650
ccttgatcca tagctttgtt totaaagtgc ctggaatgc acctatagca 700
gatgaagatc ttttgccat ctacgcacat cccaatgctc cactgtctct 750
gtcttcagaa aacttcactt ggtcttttgt caatgacac gtgaaaactc 800
ctgataaacg ttccattaca gttagcatcc totcttcaga accaacttct 850
ccatctgtga ccccttgat agtggaacca agtggatgga ttaccacaaa 900
cagtgatagc ttcactgggt ttacccttca tcaagaaaaa acaactctac 950
agcctacctt aaaattcac aataattcaa aactcttcc aaatacgtca 1000
gacccccaaa aagaaaaatg aaatacagga atagtattcg gggccatttt 1050
agtgctatt ctgggtgtct cattgcttac tcttggtggc tacttgttgt 1100
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agaaatgaac cagttctgag attagacaat gcacgggaac cttatgatgt 1200
gagtttttgg aattctagct actacaatcc aactttgaat gattcagcca 1250
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gaaagtgtca totacatcct agccttttga caaattcctc ttccaaaagg 1400
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 tttcttaca aa ttttggcca tctgagga tttactaagt agccttaatt 1550
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 aactaaaaga tttaccatt acagccctgc ctcataacta aataataaaa 1650
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 catagcccag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850
 acctgtattc tagtacgta taattttcta gatcagcaca cacatgatca 1900
 gccactgag ttatgaagct gacaatgaat gcattcaacg gggccatggc 1950
 aggaaagctg acctaccca ggaaagtaat agcttcttta aaagtcttca 2000
 aagggttttg gaattttaac ttgtcttaat atatcttagg ctccaattat 2050
 ttgggtgctt taaaaactca atgagaatca tgggt 2084

<210> 41
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
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 Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
 20 25 30
 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
 35 40 45
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val	110	115	120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser	125	130	135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr	140	145	150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser	155	160	165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val	170	175	180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser	185	190	195
Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu	200	205	210
Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn	215	220	225
Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe	230	235	240
Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu	245	250	255
Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser	260	265	270
His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu	275	280	285
Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser	290	295	300
Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu	305	310	315
Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu	320	325	330

Arg Thr Ser Val

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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gccttacgcg gcagcccgaa gattcaatat ggtgaaaato gccttcaata 100
cccttacgcg cgtgcaaaaag gaggaggcgc gccaaagacgt ggaggccctc 150
ctgagccgca cggtcagaaac tcagatactg accggcaagg agctccgagt 200
tgccacccag gaaaaagagg gctctctctg gagatgtatg cttactctct 250
taggcctttc attcatcttg gcaggactta ttgttggttg agcctgcatt 300
tacaagtaac tcatgcccaa gacacacatt taccgtggag agatgtgctt 350
ttctgattct gaggatcttg caaattccct tcttgaggga gagcctaact 400
tctgcctgt gaactgaggag gctgacatto gtgaggatga caacattgca 450
atcattgatg tgcctgtccc cagtttctct gatagtgaac ctgcagcaat 500
tattcatgac ttgaaaaagg gaatgaactg ttaactggac ttgttgctgg 550
ggaaactgcta tctgatgccc ctcaataact ctattgttat gcctccaaaa 600
aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
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gaaaaaaaaa aaaaactact accactgcaa gctcttgctc aattttagtt 1050
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cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
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ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500

tgtgttaggtg ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550

ccctataata aattttactc tatacaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50						55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

	230		235		240									
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile
			245						250					255
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu							
			260											

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 45
 gggaaatgct atctgatgcc 20

<210> 46
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 caggatctcc tcttgacgtc tgcagc 26

<210> 47
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 47
 cttctcgaac cacataagtt tgaggcag 28

<210> 48
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

caacattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

ggagaggga gggggggag gggcagccc agagcagccc cgggcaccag 50
caaggactct ctcttcacgc ccagggtgcc cccactctcg ctccattcgg 100
cgggagcacc cagtctgtg cgcacaggaa ctggctctgg gggcaccatg 150
gtttcggcgg cagccccag cctctcctc cttctgttgc tgetgctggg 200
gtctgtgct gctaccgacg ccgctctgt gccctgaag gccacgttcc 250
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gccccagccc acaaccctgg ggggcccctc accccccacc aacttctgg 400
atgggatagt ggacttcttc cgcacgtaag tgatgctgat tctgtgtgtg 450
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gaggtccccg acagagcccc cgcacagcgg ccgaggaag ccttggattc 650
ctccccag ctccaggccg acatcttggc cgcaccccag aacctcaagt 700
ccccaccag ggctgcactg ggcggtgggg accgagccag gatggtggag 750
ggcagggggg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
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cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaagg 900
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agtctcccc ggctgcacgc cctgaactgtc gggcccccaa gtggtcacct 1050
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cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150

cagaaatgct ggtccccggt gcccgggagg aatcttaccg agtgccatca 1200
 tctttacact cagcagcccc aaagggctac atctacagc acagctcccc 1250
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 aatactgctc ttaattttcc tgaagggtgg cccctgtttc tagttggctc 1450
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 caagcaccac cggcctgggg gtgagtttct cctcccgcta ctgctgctgg 1550
 gatcagggtg aatgaatgga actcttctct tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccacccctg ggaagtccga 1650
 ggggctgggg aagggtttct gacgccacgc ctggagcagg ggggcccctg 1700
 ccacccccctg ttgtccacac attgtctggc agcctgtgtc cacaatatto 1750
 gtcagctctc gacagggagc ctgggctccg tctgtcttta gggaggctct 1800
 ggcaggaggt cctctccccc atccctccat ctggggctcc cccaaactct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaacctt 1900
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu
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Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu
				20				25					30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu
				35				40					45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro
				50				55					60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly
				65				70					75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe

80										85					90				
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala					
				95					100					105					
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln					
				110					115					120					
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys					
				125					130					135					
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe					
				140					145					150					
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala					
				155					160					165					
Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr					
				170					175					180					
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp					
				185					190					195					
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys					
				200					205					210					
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro					
				215					220					225					
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu					
				230					235					240					
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly					
				245					250					255					
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro					
				260					265					270					
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val							
				275					280										

<210> 51

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

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gaaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100

gcacagagac gcagagcaag gggggcaagg aggagacct ggtgggagga 150

agacactctg gagagagagg gggctgggca gagatgaagt tccaggggac 200

cttgacctgc ctctgtgtgg acctctgact gggcagtgga gaggttgacc 250

ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
ggacatgggc tgggagacgc cctgagcgaa ggggtgggaa aggcatttgg 350
caaagagggc ggaggggcag ctggtcttaa agtcagttag gcccttgggc 400
aagggaaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
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ccttgagggc cagggccagg gcaatcctgg aggtctgggg actcctggg 700
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caacactcag ggagctgttg cccagcctgg ctatggttca gtgagagcca 850
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ggtccagca actctggggg aggcagcggc tcacagtgg gcagcagtg 950
cagtggcagc aatggtgaca accacaattg cagcagcagt ggtggcagca 1000
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ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200
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Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
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Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	325	330
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Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
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Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu	170	175	180
Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala	185	190	195
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Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala	215	220	225
Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp	230	235	240
Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala	245	250	255
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aataggggct gccctcggc tgcagtgggc taccgggga tgaagccca 3200
gcagcactgc ccaggcgagc ttacgcagca gactgacac agcagcctgc 3250
tgaggcagac ccattctggc aatggatat acccccaaac tcaccagatc 3300
acgaggggtc ccaagtctag ccgggacgag ggcctcttct tatacacaact 3350
gcccgacgac tccactcacc agtgcctgca gcccatcac gactgctgc 3400
aacgcagga gcagcctgct gctgtgggac agtcaggggt gaggagagcc 3450
cccgacagtc ctgtcctgga agcagtggtg gacccctcat ttcactcagg 3500

ggggggatgg tggttggggg ttgtggcagt tgaagaggtg gacagtcttg 3550
 actcttgcca agtgagtgga ggagactggg gtcccccagca ccccgtaggg 3600
 gctacgttag gacaggaacc tggaatgcag ctctcccccgg ggccactggg 3650
 ggtgtgtct tttgaaacac cactctctac aatttaggca gaagctgata 3700
 tcccagaaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaa 3750
 agagacagag aaaattggta tttatttttc tattatagcc atatttatat 3800
 atttatgcac ttgtaaataa atgtatatgt tttataattc tggagagaca 3850
 taaggagtcc taccogttga ggttggagag ggaaaaataaa gaagctgcca 3900
 cctaacagga gtcccccagg aaagcacccc acagggtggc gggggacaga 3950
 ctctaaact ggggctcttg cagtggcagg cgagggtgca ggaggccac 4000
 agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050
 tgagggaaca gcaaggggca cgggtatcaca gcttgagac accacacag 4100
 atggctggat cgggtgtac gggaaaacatt ttcttaagat gccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac ctccagaat 4200
 caataatccg tggcaacata ctctgtgaaa aacaaacact gtaacttcta 4250
 aataaatggt tagtcttccc tgtaaaa 4277

210 58

211 1115

212 PRT

213 Homo sapiens

400 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu
1				5				10					15	

Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
			20					25					30	

Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
			35					40					45	

Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
			50					55					60	

Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
			65					70					75	

Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
			80					85					90	

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln	95	100	105
Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala	110	115	120
Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln	125	130	135
His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys	140	145	150
His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val	155	160	165
Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met	170	175	180
Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu	185	190	195
Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val	200	205	210
Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr	215	220	225
Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile	230	235	240
Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser	245	250	255
Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser	260	265	270
Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665					670					675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680					685					690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695					700					705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710					715					720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725					730					735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740					745					750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755					760					765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770					775					780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785					790					795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
				800					805					810	
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
				815					820					825	
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
				830					835					840	
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
				845					850					855	
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	951	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 53

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gaggc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
cacccaaaag cccaggctccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<221>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgaggaggctg ggctgctatg atccggaccc cattgtcgga ctctgcccat 50
cgactgctcc tcccaggctc ccggggcgga ccccgcgga acatgcagcc 100
cacgggcccc gaggggtccc ggcgcctcag ccggcggtat ctggggcgtc 150
tgtgtgctcc gctaactgtg ctgatgtgc ggcagcccg aaacggcgcg 200
gagaccagcc cggggcgccc cagagccctc tccacgtgg gctccccag 250
cctcttcacc accgcgggtg tcccagcgc cctcactacc ccaggctca 300
ctacgcagg cacccccacc acctggacc ttgggggtcg cgggcaggcc 350
ctgatgcgga gtttccact cgtggaagg cacaatgacc tgcgccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacagga ttagagagg cctcgtgggt 500
gcccagttct ggtcagcctc cgtctcatgc cagtcaccag accagactgc 550
cgtgcgcctc ggcctggagc agattgacct cattcacgc atgtgtgct 600
cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
cagcctctct gtgtgcgca gttctatgt gctgggggtg cgtacactga 750
cacttacctt cactgcagt acaccatgg cagagagttc caccagttc 800
agacaccaca tgtacacca cgtcagcgga ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc ggcgtgggcac gatgatagat ttgtccatag 900
 catcggacac cttgataaga aggggtccctgg aagtgtctca ggcctccctg 950
 atctttctccc actcagctgc cagagctgtg tctgacaatt tcttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcacc gtgatgggta 1050
 caactgtccat ggggggtgctg cagtgcacac tgcctgctaa cgtgtccact 1100
 gtggcagacc actttgacca catcagggca gtcattggat ctgagttcat 1150
 cgggatttgtt ggaaattatg acgggaactgg ccgggtccct caggggctgg 1200
 aggatgtgtc cacataccca gtccgtgatag aggagttgct gactcgtasc 1250
 tggagcgagg aagagcttca aggtgtccct cgtggaaacc tgcctgggggt 1300
 ctccagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactccac 1400
 ctctgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaaccaat cgggtccctt ggaggctctc aaatgcctcc ccataccttg 1500
 ttccaggctt tctggctgct gccaccatcc caaccttcc ccagtggctc 1550
 tcttgacaca gtccgtcccc gcagaggtca ctgtggcaaa gctcacaaa 1600
 gccccctctc ctagtctcatt cacaagcata tcttgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 437
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
 1 5 10 15
 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro			
				65					70					75			
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser			
				80					85					90			
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg			
				95					100					105			
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe			
				110					115					120			
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val			
				125					130					135			
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp			
				140					145					150			
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His			
				155					160					165			
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala			
				170					175					180			
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val			
				185					190					195			
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser			
				200					205					210			
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys			
				215					220					225			
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met			
				230					235					240			
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val			
				245					250					255			
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala			
				260					265					270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Gln	Val	Ser	Gln	Ala	Pro			
				275					280					285			
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu			
				290					295					300			
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly			
				305					310					315			
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu			
				320					325					330			
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg			
				335					340					345			

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
	350	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
	365	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
	380	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
	395	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
	410	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
	425	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
	440	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
	455	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
	470	480
Thr Phe Thr Gln Trp Leu Cys		
	485	

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 64
 ccttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 4"

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgtataggctc tgtccacaaa tgcacccag agcaggagct gaaagcctct 50
aacaccccaca gatccctcta tgactgcaat gtgaggtgtc cggcttttgc 100
ggcccagcaa ggcgtataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcacc cagctgaagc caacaagagt tctgaagata 200
tcgggtgcaa atgcctctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtgggtga 300
gcccattgca gtgcctggcc atgacgtgga ggctactgc ctgctgtgog 350
agtgcaggta ccaggagcgc agcaccacca ccaccaaggt catcattgtc 400
atctacctgt ccgtgggtggg tgcctgttg ctctacatgg ccttctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacaat gagcaactgc 500
acaatgagga ggagaatgag gatgctcgtc ctatggcagc agctgctgca 550
tccttcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaagtgc 600
ccagcagcgg tgggaagtgc aggtgcagga gcagcgggaag acagtcttcc 650
atcggcacia gatgctcagc tagatgggct ggtgtgggtg ggtcaaggcc 700
ccaacaccat ggctgcagc ttccaggctg gacaaagcag ggggtctact 750
ctccttctcc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
ctccttctcc ctaactttag aaatgttgta ctggctatt ttgattaggg 850
aagagggatg tggctctctga tctctgttgt cttcttgggt ctttgggggt 900
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
ctcaggagtg gatgcgatct gtctctctct gctccactct tgcgccttc 1000
cagctctgag tcttgggaat gttgttaacc ttggaagata aagctgggtc 1050
ttcaggaaat cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
gttcttttct gcagtggttc ttatcaccac ctccctccca gccccgggc 1150

ctacagcccca gccccagctc cagccctgag gacagctctg atgggagaga 1200
 tgggccccct gagcccaactg ggtcttcagg gtgcaactgga agctgggtgt 1250
 cgtgttcccc tgtgcaacttc tgcactggg gcatggagtg cccatgcata 1300
 ctctgctgcc ggtccccctca cctgcaacttg aggggtcttg gcagtccttc 1350
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 gactcgagga tgagcgtgga tctgaacacc acagcccttg taattgggtt 1450
 gctctttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tctctttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 ttttatttct ctca 1564

<210> 63
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
 170 175 180

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 aggggggtctc gtttgggttc cgctaatttc tgtcctgagg cgtgagaactg 50
 agttcatagg gtccctgggtc ccggaaccag gaagggttga gggaacacaa 100
 totgcaagcc ccgcgcaccc aagtgagggg ccccggtgtt gggtccctcc 150
 tcccttttga tcccacccc tcgggggttt ggttcttctt ggggaccccc 200
 tcggggggag atggccgcgt tgatggggag caaggattcg tctgctgccc 250
 tgcctctact ggccggcgtg ctgatgggtg agagctcaca gatcggaagt 300
 tcggggggca aactcaactc catcaagtc tctctggggc gggagacgcc 350
 tggtcaggcc gccaatcgat ctgggggcat gtaccaagga ctggcattcg 400
 ggggcagtaa gaaggggaaa aacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcgggcctgc atggtgtgtc ggagaaaaaa gaagcgcctgc caccgagatg 550
 gcatgtgtgt ccccagtaac cgtgcgaata atggcatctg tatccagtt 600
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650
 cagagatcga aaccacggtc attactcaaa ccctgacttg gcatggcaga 700
 atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
 gaacccctgcc taagatcacg agactgcatt gaagggtttt gctgtgctcg 800
 tcattttctgg accaaaatct gcaaacccag gtcccatcag ggggaagtct 850
 gtacaaaaca acgcaagaag ggttctcatg ggctggaaat ttccagcgt 900
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<210> 70
 <211> 259
 <212> PRT
 <213> Homo sapiens

<400> 70
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 35 40 45
 Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130					135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
				245					250					255
Cys	Gln	Lys	Ile											

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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 ctgaaaaga 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<430> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

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Ser Ser Tyr Asp	Gln Ser Ser Val His	Asn Arg Ile Pro Tyr Gln			
	290		295		300
Ser Pro Val Ser	Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn				
	305		310		315
Gly His Gly Gly	Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr				
	320		325		330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg				
	335		340		345
Lys Arg Ile Ala	His Val Met Trp Lys Thr Pro Val Gly Gln Trp				
	350		355		360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 73
 aaattcatggc aaatatttcc ctcccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 74
 tggtaaaactg gcccaaaactc gg 22

<210> 75
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 75
 ntaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

0411> 76

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 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 77
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 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
 35 40 45
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
 50 55 60
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
 65 70 75
 Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

02100 78

02110 2143

02120 DNA

02130 Homo sapiens

04000 78

cgccggaggc agcggggggc tggcgcagcg ggcacatggc cgttgtctca 50

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cgccccctgg cctgcagagg ccgaggagcc gcttctgtgg cacatacatc 200

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<110> 79
 <111> 475
 <112> PERT
 <113> Homo sapiens

<100> 79
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 Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
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 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
 35 40 45
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
 50 55 60
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
 65 70 75
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
 80 85 90
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
 95 100 105
 Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135

Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	
				140					145					150	
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	
				155					160					165	
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	
				170					175					180	
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	
				185					190					195	
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	
				200					205					210	
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	
				215					220					225	
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	
				230					235					240	
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	
				245					250					255	
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	
				260					265					270	
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	
				275					280					285	
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	
				290					295					300	
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	
				305					310					315	
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	
				320					325					330	
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	
				335					340					345	
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	
				350					355					360	
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	
				365					370					375	
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	
				380					385					390	
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys	
				395					400					405	
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser	
				410					415					420	

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430					435
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 81
 ggttaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 83
 <211> 1844
 <212> DNA
 <213> Homo sapiens

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<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195

Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr	200	205	210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala	215	220	225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr	230	235	240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp	245	250	255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro	260	265	270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala	275	280	285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln	290	295	300
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala	305	310	315
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile	320	325	330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg	335	340	345
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg	350	355	360
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn	365	370	375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu	380	385	390
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala	395	400	405
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu	410	415	420
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp	425	430	435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser	440	445	450
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu	455	460	465
Lys	Asp	Asp	Trp	Thr	Val	Pro	Tyr	Gly	Arg	Ile	Tyr	Phe	Ala	Gly	470	475	480

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
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Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
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 <211> 3316
 <212> DNA
 <213> Homo sapiens

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 gaactcagag ccgggaagcc ccattcact agaagcactg agagatgcgg 200
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 cttctcagat gccaaagact tgtatgaggt ttccaaaaga ggaactcgtg 500
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25				30	

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile	50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys	65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg	80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val	95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn	110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu	125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu	140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys	155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His	170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala	185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr	200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu	215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile	230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu	245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro	260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu	275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe	290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys	305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr			

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His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	335		340		345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr	350		355		360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365		370		375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380		385		390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395		400		405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410		415		420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425		430		435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440		445		450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455		460		465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470		475		480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485		490		495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500		505		510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515		520		525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530		535		540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545		550		555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560		565		570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575		580		585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590		595		600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu					

605	610	615
Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His		
620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp		
635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly		
650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile		
665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr		
680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser		
695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly		
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Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu		
725	730	735
His Ile Gln Asp		

<210> 37

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 37

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cccccatca agccctttgg ggcctgggaag aagcggagct ggtaccttac 200

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atcttgaca ctggggagac catcagtga gccaatgaag accagagccc 350

agagcaagac tatgatgagg ccttagggcg cctggagccc ccacggggca 400

gaggcagttg tcccggggcg gtctgggaag tagaggtgta ttcaagtgcg 450

agcaaaagtat atgtggcagt gcatggcacc acggtgctgg aggatgaggg 500

ccgggagcag ggcgggggca tccatgtcat tgtctcaac caggccacgg 550

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<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105

Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu	110	115	120
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val	125	130	135
Leu	Asn	Gln	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Asp	140	145	150
Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn	155	160	165
Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Cys	Thr	Val	Lys	Asp	Glu	170	175	180
Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser	185	190	195
Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp	200	205	210
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His	215	220	225
Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu	230	235	240
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	245	250	255
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser	260	265	270
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr	275	280	285
Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu	290	295	300
Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn	Tyr	Leu	305	310	315
Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro	320	325	330
Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met	335	340	345
Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro	350	355	360
Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys	Ala	Ser	365	370	375
Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe	Ala	Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	
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Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr	
				410					415					420	
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	
				425					430					435	
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly	
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Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys	
				455					460					465	
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg	
				470					475					480	
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val	
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Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly	
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Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val	
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Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala	
				530					535					540	
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu	
				545					550					555	
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr	
				560					565					570	
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp	
				575					580					585	
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp	
				590					595					600	
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe	
				605					610					615	
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro	
				620					625					630	
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu	
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<212> DNA
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

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 <220>
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 <400> 90
 cctcaacacag gccacggggc ac 22

 <210> 91
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 <223> Synthetic oligonucleotide probe

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 <210> 92
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 <210> 94
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 <212> DNA
 <213> Homo sapiens

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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
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 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210

Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	
				215					220					225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	
				230					235					240	
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu	
				245					250					255	
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly	
				260					265					270	
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg	
				275					280					285	
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile	
				290					295					300	
Leu	Ser	Val	Gly	His	Gln	His									
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<210> 96

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 96

gttgtgggtg aataaaggag ggcag 25

<210> 97

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 97

ctgtgctcat gttcatggac aactg 25

<210> 98

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

ggatgatttc atctccatta gctgtctgtc tctggctatg ttggtgggat 50

<210> 99

<211> 1429

<212> DNA

<213> Homo sapiens

<410> 99

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gaaatgtact aaataaaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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				20					25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
				35					40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
				50					55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
				65					70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
				80					85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
				95					100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
				110					115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
				125					130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
				140					145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
				155					160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
				170					175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
				185					190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
				200					205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
				215					220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
380	385	390
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<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
				215					220					225	
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
				230					235					240	
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	
				245					250					255	
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
				260					265					270	
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp	
				275					280					285	
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
				290					295					300	
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
				305					310					315	
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
				320					325					330	
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
				335					340					345	
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	
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Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	
				365					370					375	
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
				380					385					390	
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
				395					400					405	
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
				410					415					420	
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
				425					430					435	
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
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				470					475					480	
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	
				485					490					495	
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
				500					505					510	
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
				530					535					540	
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
				545					550					555	
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
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Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
				575					580					585	
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
				590					595					600	
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
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His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
				620					625					630	
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
				635					640					645	
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
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Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
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Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
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Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
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Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
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Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
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Val Ser Gly Ala	Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val		755	760	765
Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu		770	775	780
Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr		785	790	795
Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly		800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala		815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu		830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile		845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu		860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe		875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr		890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile		905	910	915
His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser		920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala		935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp		950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro		965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu		980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe		995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu		1010	1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg
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Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe
 1040 1045 1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly
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Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe
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<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
381 385 390

Gly Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

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425 430 435

Leu Tyr Val Gln Met Glu Asn
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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

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<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 106

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<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 107

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<210> 108

<211> 25

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

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cacttgacac ttaccatgtt ctgcacccgc agtggggaca gccacagacg 700
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ctcaaggcct cgtttccttc tggggcctct ggtggggaga ccccaagacc 800
cccgaactgt acaagcaggt gtcgcctttt gtggcctgga tctgggaact 850
ggttcggggg agcagtcccc agcccgggcc cctgcctggg accaccaggc 900

cccaggaga agcgcgcctga gccacaaact tggggatga aaatgagatg 950
 ggcgcctcag gcctggaatg ttccgtgggt gggcccccag ggaagcctga 1000
 tgttcagggg tgggggtggga cgggcagcgg tggggccacac ccattccaca 1050
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 aaaaaaaaaa gaaa 1114

<210> 111
 <211> 283
 <212> PRT
 <213> Homo sapiens

<403> 111
 Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
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 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
 35 40 45
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
 50 55 60
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
 65 70 75
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
 80 85 90
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
 95 100 105
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
 110 115 120
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
 125 130 135
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
 140 145 150
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
 155 160 165
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
 170 175 180
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
 185 190 195
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

	200		205		210
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg					
	215		220		225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly					
	230		235		240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val					
	245		250		255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly					
	260		265		270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala					
	275		280		

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 112
 gacgtctgca acagctcttg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 113
 agagaagqaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 114
 tgaacattac catgtcttgc accgcagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgcgc actccggacg 50

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cgctgtccgc gctgggcaag gttagcaggcg ccgcctgtct gctcaaggac 150
tatgtcacgc gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200
ggtcactgtg acggggcgca acacaggcat cgggaagcag accgccttgg 250
aaatggccag gagaggagcg aacatcctcc tggcctgcgc agacatggag 300
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
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tgtgggacaa gctgaaagcc tcagccctct cggggtcat caacctctcg 600
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gcctgtccgg gagggttcca aggtgtccg tgaagagcat gggcaagttg 1450

tctgacacit ggtggattct tgggtccctg tgggaccttg tgcattgcctg 1500
 gtcctctctg agccttgggtt tcttcagcag tgagatgctc agaataactg 1550
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 ggtgtgctcg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650
 gagagcaggt gcaggtgtca tcccgagttc aggtctctga cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggaactc 1750
 cacttctcta tcaattctca tggtagtcca aactgcagac tctcaaacct 1800
 gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala
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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys
				20					25					30

Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly
				35					40					45

Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg
				50					55					60

Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys
				65					70					75

Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His
				80					85					90

Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg
				95					100					105

Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile
				110					115					120

Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr
				125					130					135

Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His
				140					145					150

Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala
				155					160					165

Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly
				170					175					180

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					191					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	
				230					235					240	
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
				245					250					255	
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
				260					265					270	
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
				275					280					285	
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
				290					295					300	
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
				305					310					315	
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	
				320					325					330	

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
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 ctggcggtgc tggcgctcgg gacaggagac ccagaaaagg ctggcgctcg 100
 gggcgacacg ttctggggc tgaccagcgt ggcccgcgcc ctggcgcccg 150
 agcgccggct gctggggctg ctgaggcggt aactcgcgcg ggaggaggcg 200
 cggctggcgg aactgactag attctaagac aaggtacttt ctttgcctga 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atggcgctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
agagtcaatg gctctgcaat caatgacctg tacagcccca aacggctctt 550
ttctctcaca ggggatgaat gattccaagt tggcaagggtg goctatgaca 600
tggtggatta ttaccatgac attccatggc tggaggaggc tgtcagtctc 650
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700
agatgccttg gataccttgg cctttgotta ttccgggcca ggaaatgttt 750
cgtgtgcctt cagcctctct cgggagtttc ttctctacag ccagataat 800
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
ccccaaccac gtggtagctg aggtctgcat ccagaggccc aatatacccc 900
acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
cagccactc totaccagat ccttagcttc tactgttctt atgagacca 1000
ttccaagccc tactgtctg tccagcccat ccggaaggag gtcacccacc 1050
tgagaccta cattgctctc taccatgaat tctcagtga ctcagaggct 1100
cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtggaggc 1150
atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
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ggtggtgaa tatggcatcg gaggacacta tgagccctac ttgacccatg 1350
ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccagatt 1400
gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
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tttgggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttc 1550
gctggctgtc ctgtcctggg gggagataag tgggtggcca acaagtggat 1600
acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
actgaaactgt tggcagagag aagctgggtgg agtctgttgg ctttcagag 1700
aagccaggag ccaaaagctg gggtaggaga ggagaaagca gacagcctc 1750
ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800
gggagagggtt gttaccaggg gacactgaga atgtacattt gatctgcctc 1850

agccacggaa gtcagagtag gatgcacagt acaaggagg ggggagtga 1900
 ggctgagag ggaagttttt ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt cagatcagtg ggtcttttgg caatttgaac 2000
 ctgacacaca gggacacaaga agtggcaata aggcacactg caggaggggg 2050
 tagctgact ccagaaactt taagactttc tcccaactgc cttctgctgc 2100
 agcccaagca gggagtgttc cctccacaga agcatatccc agatgagtgg 2150
 tacattatat aaggattttt ttaagttag aaacaacttt cttttctttt 2200
 tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

(210) 118
 (211) 544
 (212) PRT
 (213) Homo sapiens

(400) 118
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
 1 5 10 15
 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
 20 25 30
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
 35 40 45
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
 50 55 60
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
 65 70 75
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
 80 85 90
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
 95 100 105
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
 110 115 120
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
 125 130 135
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
 140 145 150
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
 155 160 165
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
 170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser
530 535 540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

ggggagagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

gggcaagtga tccaaggcat ctts 24

<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgaggggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<433> 122

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gaatcggccc tggcaggttg ggcacagagc gctggctgag ggacccagcc 150
ggagagcccc ggagcccccg taaccccgcc ggggagccgc caggatgccg 200
cgccgggaat cggagcaggt gcgtactgc gggcgcttc cctacctctg 250
gctcaagttt tcaattatca tctattccac cgtgtttctg ctgattgggg 300
ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccctg aaagtgcctt cctggctcca gccatcacc tcatcctct 400
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gaccattgac tctctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggaactccaa aacatcattg accttgttca gaaaaagttc 650
aagtgtgtg ggggggagga ctaccgagat tggagcaaga atcagtacca 700
cgaactgcagt gccctcggac cctcggcctg tggggtgccc taccctcgt 750
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 tcttgagccc tagttttttt ttaactgatt ttgttaacat tcattttttt 1650
 gtacagataa caggagtttc tgactaatca aagctgggtat ttcccgcgat 1700
 gtctattctt tgcctctccc ccaaccagtt tgttaatcaa acaataaaaa 1750
 catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123
 <211> 294
 <212> FRT
 <213> Homo sapiens

<400> 123
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 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly

	170		175		180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn					
	185		190		195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val					
	200		205		210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile					
	215		220		225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly					
	230		235		240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr					
	245		250		255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp					
	260		265		270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly					
	275		280		285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn					
	290				

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 124
 atcatatt ccacgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 126

ctgtgtgtgtt ggcatttatg cagaggttga ggggcagaaa tataaaaacc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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gttgccctct gacacctggg aagatggag gcccgaggac ctacacctt 100

ctctgtgggt tgcctggcag cactctgac caagccacc tcagtccac 150

tgcagttctc atctctgggc caaaagtcac caaagaaaag ctgacacagg 200

agctgaagga ccacaaagcc accagcacc tgcagcagct gccgtgtct 250

agtgcacatg gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300

ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta 350

acatctcca gctgcaggtg aagcctcgg ccaatgacca ggagctgcta 400

gtcaagatcc cctggacat ggtggctgga ttcacacgc cctggtcaa 450

gaccatcgtg gagtccaca tgaagactga ggcacaagcc accatccga 500

tggacaccag tgaagtggc cccaccgcc tggctctcag tgaactgtgc 550

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caacatcccg ttcagctcca tctgagtcca ggaagtgggt aaagctgcag 950

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<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
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 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170	175	180
Ala Lys Gln Val Met Asn Leu Leu Val	185	Pro Ser Leu Pro Asn Leu	195
Val Lys Asn Gln Leu Cys Pro Val Ile	200	Glu Ala Ser Phe Asn Gly	210
Met Tyr Ala Asp Leu Leu Gln Leu Val	215	Lys Val Pro Ile Ser Leu	225
Ser Ile Asp Arg Leu Glu Phe Asp Leu	230	Leu Tyr Pro Ala Ile Lys	240
Gly Asp Thr Ile Gln Leu Tyr Leu Gly	245	Ala Lys Leu Leu Asp Ser	255
Gln Gly Lys Val Thr Lys Trp Phe Asn	260	Asn Ser Ala Ala Ser Leu	270
Thr Met Pro Thr Leu Asp Asn Ile Pro	275	Phe Ser Leu Ile Val Ser	285
Gln Asp Val Val Lys Ala Ala Val Ala	290	Ala Val Leu Ser Pro Glu	300
Glu Phe Met Val Leu Leu Asp Ser Val	305	Leu Pro Glu Ser Ala His	315
Arg Leu Lys Ser Ser Ile Gly Leu Ile	320	Asn Glu Lys Ala Ala Asp	330
Lys Leu Gly Ser Thr Gln Ile Val Lys	335	Ile Leu Thr Gln Asp Thr	345
Pro Glu Phe Phe Ile Asp Gln Gly His	350	Ala Lys Val Ala Gln Leu	360
Ile Val Leu Glu Val Phe Pro Ser Ser	365	Glu Ala Leu Arg Pro Leu	375
Phe Thr Leu Gly Ile Glu Ala Ser Ser	380	Glu Ala Gln Phe Tyr Thr	390
Lys Gly Asp Gln Leu Ile Leu Asn Leu	395	Asn Asn Ile Ser Ser Asp	405
Arg Ile Gln Leu Met Asn Ser Gly Ile	410	Gly Trp Phe Gln Pro Asp	420
Val Leu Lys Asn Ile Ile Thr Glu Ile	425	Ile His Ser Ile Leu Leu	435
Pro Asn Gln Asn Gly Lys Leu Arg Ser	440	Gly Val Pro Val Ser Leu	450
Val Lys Ala Leu Gly Phe Glu Ala Ala		Glu Ser Ser Leu Thr Lys	

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
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Pro Val Ser Gln

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<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 150

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	20	25	30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met	35	41	45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys	50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile	65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys	80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg	95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp	110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser	125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg	140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln	155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val	170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu	185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met	200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys	215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg	230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn	245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His	260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu	275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys	290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser			

305

310

315

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Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

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<010> 132
 <011> 536
 <012> PRT
 <013> Homo sapiens

<400> 132

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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	20	25	30	35
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	35	40	45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	50	55	60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	65	70	75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	80	85	90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	95	100	105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	110	115	120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	125	130	135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	140	145	150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	155	160	165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	170	175	180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	185	190	195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	200	205	210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	215	220	225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	230	235	240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	245	250	255	

Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	260	265	270
Gln	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	275	280	285
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	290	295	300
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	305	310	315
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	320	325	330
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	335	340	345
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	350	355	360
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	365	370	375
Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Glu	Thr	Phe	Lys	380	385	390
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser	395	400	405
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg	410	415	420
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile	425	430	435
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr	440	445	450
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln	455	460	465
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val	470	475	480
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile	485	490	495
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln	500	505	510
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln	515	520	525
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val					530	535	

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<212> DNA
<213> Homo sapiens

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<210> 134
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<400> 134
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 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
 50 55 60
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
 65 70 75
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
 80 85 90
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
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 Val Phe Cys Gln Gln Ser Arg Ala Lys Asp Arg Val Ala Val Ala
 110 115 120
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
 125 130 135
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
 140 145 150
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
 155 160 165
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
 170 175 180
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
 185 190 195
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
 200 205 210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
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Leu Thr Gly Tyr Val
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<210> 135
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 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcatcgc tcccgctggc tcagaacctt ggcctgtgca gccggcaccc 150
 aggtgtggag acaagatcta caaccccttg gaggagtgt gttacaatga 200
 cgcacatcgt tccctgagcg agaaccggca atgtgggtcc cctgcacct 250
 tctggccctg ctttgagctc tctgtctctg attccttttg cctcacaac 300
 gattttgttg tgaagctgaa ggttcagggc gtgaattccc agtgcacac 350
 atctccatc tccagtaaat gtgaaagcag aagacgtttt cctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagg cattgtatgg ccctgtgtgg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	66		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
			95						100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
			110						115					

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 agtggccccc atgaactcctt acctgatgct gtgccagcca cacaagagat 150
 ctgggggacaa gttctaagac cccctgcagc actgtttgcta tgatgatgac 200
 ctctgtgcctt tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250
 ctgttttgag cagtgtctgc cctggacctt catggtgaag ctgataaacc 300
 agaaactgga ctccagcccg accctggatg acaggctttg tcgcagtgtc 350
 agctaattga acatcagggg aaagatgaat cctggattct ccttctgagg 400
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 gacctgtctg aggcacaccc tgcagtgcg ctgaggaggg ccacaggtcc 550
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 ggaacttgaa cctctctgat gacccctatg gccaacatca acccggcacc 650
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 atctcaagtt ctctctctac caggagcaaa gcacaggatc ataataaatt 750
 catgtacttt ataaatgaaa a 771

<210> 133
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1 5 10 15

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				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
			35						40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139
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 ctgcgcgcga ccagaaattc ctctgcgcgc ccgacgggga catgggcgctc 150
 ccacgggcgc tggaggcgcg cagctgggcg tggggatccc tgcctcttcgc 200
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ygaatcctct gctcccccct catcctgtct ctggtctaca agcaaaaggca 800
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 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

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				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttctgtgc ctcttttctt gccacacgct gcttctgtgc 150
 ccttctccga ccccgctcta gcagcagacc tctgtgggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccggt accagcgggc tgacctggg gaaaggatgg tcccgaggt 300
 gaggtctctc tctctcttgc tgggaactgc gctgctctgg tcccccctgg 350
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 agatactccc ccggcgagag ctggcacccc taattggagc cacaaggcct 450
 gatgtactgc ctgcgtgtga ctgtctcaga gggcgcccat gtgagttgtt 500
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 cagcaatgct gtcccaagtg tgttgaaact cactctct ctggactcag 600
 ggcaccacca aagtcctgac agcacaaagg gacctgtac caacacggag 650
 agatcttcag tgccatgag ctgttccctt ccgctctgac caaccagtgt 700
 gtctctgca gctgcacaga gggccagatc taatggggcc tcacaacctg 750
 ccccgaaaca ggtgcctag caccctccc actgcagac tctgtctgac 800
 aagcctgcaa agatgaggca agtgagcaat ccgatgaaga ggacagtgtg 850
 cagtcctcc atgggggtgag acatctcag gatccatgtt ccagtgtgc 900
 tgggagaaaag agaggcccg gcaccccagc ccccactgga ctacggccc 950
 ctctgagctt catctctgc cacttcagac ccaagggagc aggcagcaca 1000
 actgtcaaga tctctctgaa ggagaaacat aagaaagcct gtgtgcctgg 1050
 cgggaagaag tactcccaag gggaggtgtg gcacccggcc ttcctgctt 1100

tagggccctt gccctgcctc ctatgcacct gtgaggatgg ccggccaggac 1150
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 agtggctggg aagtgcctga agatttgccc agaggacaaa gcagacctg 1250
 gccacagtga gatcagttct accaggtgtc ccaaggccacc gggccgggtc 1300
 ctggtccaca catcgttctc cccaagccca gacaacctgc gtcgctttgc 1350
 cctggaacac gaggcctcgg acttggttga gatctacctc tggaagctgg 1400
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
 ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500
 aagacttcca gaaagaggca cagcacttcc gactgcctgc tggcccccac 1550
 gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<R10> 142

<R11> 451

<R12> PRT

<R13> Homo sapiens

<R40> 142

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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	
				290					295					300	
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	
				305					310					315	
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	
				320					325					330	
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	
				335					340					345	
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	
				350					355					360	
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	
				365					370					375	
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	
				380					385					390	
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	
				395					400					405	

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
 425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cttggggaaa atgctgatct cagtgcgaat gctggggcgca ggggctggcg 150
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 ggcgcagcgg ggaggtcacc gtgagacggg acttgccctc gtggggcgccg 400
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 ccaggggaga gtcgggacgg agataccatg ccaggactct cgggggtcct 500
 gtgagctgac gtccgggtgag cacttttccc ccaaaccttg gactgactgc 550
 tttaaggctc gcaaggcggg ccagggcgca gacggagctc ggatgtgggt 600
 aaotgaaaga accaataaaa tcatgttctt ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> FFT
 <213> Homo sapiens

<400> 144
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90

Arg Ser Pro

<210> 145
 <211> 1383
 <212> DNA
 <213> Homo sapiens

<400> 145
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 aacgcgaact agtctgttta gaggaacggc tggcccagtg ccaggaccag 250
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 aacccaacag tggtagacag ctccagttat ccaggagagg ggtgatccc 900

cccctacggc ttgacagcag acacctacat cgacctggta gatgatgagg 950
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 aaagccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
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 ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500
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 ttccctcctg ctctcctgcc ccattgtcaac aaatttcagg ctaaggatgc 1600
 ccagaccca gggctctaac cttgtatgag ggcaggccca gggagcaggc 1650
 agcagtgttc ttccctcag agtgacttgg ggaggagaa ataggaggag 1700
 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
 aacaggactt totccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PFT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25						30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35				40						45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn

50										55					60				
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala					
				65					70					75					
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu					
				80					85					90					
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro					
				95					100					105					
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys					
				110					115					120					
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys					
				125					130					135					
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg					
				140					145					150					
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln					
				155					160					165					
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala					
				170					175					180					
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala					
				185					190					195					
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr					
				200					205					210					
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro					
				215					220					225					
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln					
				230					235					240					
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser					
				245					250					255					
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala					
				260					265					270					
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala					
				275					280					285					
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys					
				290					295					300					
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro					
				305					310					315					
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr					
				320					325					330					
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile					

335

340

345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

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gtttctctct tctctctaat ccctccgtca cctctctctgt cctccgtttc 150

cctgcctgtg ggctccattca cagaacacat ccctggctct cctgctcagt 200

ctggctctga gtctctctca gctgggatca gggcagtggc aggtgtttgg 250

gcacagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctct 300

gtttctctgt tcttaagacc aatgcagagg ccctgggaagt gcggtttctc 350

agggggccagt tctctagcgt ggctccctc tacagggaag ggaaggacca 400

gcattttatg cagatgcacc agtatcaagg caggacaaaa ctggtgaagg 450

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aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val Gln Ala	20 25 30
Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser Pro Lys	35 40 45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly Gln Phe	50 55 60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln Pro Phe	65 70 75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val Lys Asp	80 85 90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn Ile Thr	95 100 105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser Gln Ser	110 115 120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala Leu Gly	125 130 135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg Asp Ile	140 145 150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro Thr Ala	155 160 165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp Ser Arg	170 175 180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile Ser Leu	185 190 195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met Arg His	200 205 210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile Gly Asp	215 220 225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys Val Leu	230 235 240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	245 250 255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	260 265 270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	275 280 285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	

290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val		
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val		
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp		
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His		
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr		
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr		
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe		
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg		
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn		
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu		
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu		
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu		
485	490	495
Pro Arg Gly Glu Met		
500		

<310> 149

<311> 24

<312> DNA

<313> Artificial Sequence

<320>

<323> Synthetic oligonucleotide probe

<400> 149

gggtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 150
ggaaatgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 151
gcagatgaca cagtatcaag gcaggacaaa actggtgaag gatto 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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ggtcggattg caacgaggag aagatgaatg accaacggac tgggtgaatg 100
aatgaatggc ggagccggag cgcgcctgag gagcctggcg agcctggggc 150
gcctcgccct gttgtgtgc gcgcgcgcgc ccgcgcgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtgggcgc ggggcgcgcg ggcaggtgga 250
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cacccctctt tggggagctg ctggacccct tccaccacc ttccaggcgc 450
cgctcggccc ctgcgcgacc acccttcggc cggcggaacg cacttcgacc 500
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gcatgtgac tgtagtccac atggagctct cagcatacag tgcaacaggt 900
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agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
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Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
20 25 30

Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
125 130 135

Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
155 160 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro
170 175 180

Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn
185 190 195

Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr
200 205 210

Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys
215 220 225

Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu
230 235 240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
 245 250 255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 154
 aactgctctg tgggtggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ctggacctg agcagcttct tgggccttgg tacgtgcttg cgggtggcctc 150
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaaac tgcggacgct gtctctcag 250
 cccgggctgg gagggtgtga ccagaagtgt atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggggtgtg gagctctggg 351
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 agccagccag gaggccatgg ggcctttcac caagtggagc aggagcctgg 500
 gcttctgttc acagtacagc gccagctgc agaaggacct cactgtgt 550
 cacaagatcc ttctgtgagt gctgctccc cagtagggat gggtccaca 600
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 gggccacaga ccagctcaga ataaagcgt tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
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 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90
 Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
 95 100 105
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
 110 115 120
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
 125 130 135
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
 140 145 150
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
 155 160

<210> 159

<211> 1665
<212> DNA
<213> Homo sapiens

<400> 159

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gtccatgtgc cctgctcctt ctccatcccc tcgcctgggt ggatttcccc 200
tggcccagta gttcatgggt actggttccg ggaagggggc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctggggcagt gtgggaggag 300
actggggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcacc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggtgccccc agaactgac ctgctctgtg cctggggcct 550
gtgagcaggg gacacccct atgatctctt ggataggga ctcctgtctc 600
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 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtata 1600
 tcaaacctga atccacactg tgcctccct tttatttttt taactaaaag 1650
 acagacaaat tcta 1665

<210> 160

<211> 463

<212> PRT

<213> Hcmo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	110	115	120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	125	130	135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	140	145	150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	155	160	165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	170	175	180	

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala	410	415	420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser	425	430	435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu	440	445	450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg	455	460	

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgccagtg gacctgcaga ggtcggcaga acagagctct ggagatgaag 50
 acctgttcc tgggtgtcac gctcggactg gcgctgcac tgtccttcac 100
 cctggaggag gaggatata cagggacctg gtactgaag gccatggtgg 150
 togataagga ctttcggag gacaggagga ccaggaaggt gtccccagtg 200
 aaggtgacag cctcggggcg tgggaagttg gaagccactg tcaccttcac 250
 gagcagggat cgggtgcacc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcaca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcttg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 acccggagga cctggaagaa tttaagaaat tgggtgcagg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct ggccttcaga 550
 acactaggca gccccgggt ctgcacctcc agagccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcctt 650
 gctccaccac acctgacct aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
 20 25 30
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
 35 40 45
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
 50 55 60
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
 65 70 75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
155 160 165

Cys Val Pro Glu His
170

<210> 163

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

gtcttcggga aagtccttat c 21

<210> 166

<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gactagtgtt cgggaacgca gcttc 25

<210> 167
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggacctg gtaagtgaag gccatggtgg tcgataagga ctttcggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtcttcca ccttggagga ggaggatata acagggaact ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gttcgcgaga tgcagagggt gaggtggctg cgggaactgga agtcacggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgctcc tccccctcc 100
aggccatgag gattctgcag ttaactctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttgagtgca agctcactc 200
ccajccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250
cgagctcat cgcgccca ga tggctctga cagcagccca ctgcctcaag 300
cccgctaca tagtcaact ggggcagcac aacctcaga aggaggagg 350
ctgtgagpag acccggacag ccactgagtc ctccccccac ccggcttca 400
acaacagct ccccaacaaa gaccacgca atgacatcat gctggtgaag 450
atggcctgca cagtctcat cactgggtgt gtgcagcccc tcacctctc 500

ctacagctgtg gtacatgtgtg gaaccagctg cctcatttcc ggcctggggca 550
 gaaggtccag cccccagtta ggcctggctc acacattggg atgggcacaa 600
 atcaccatca ttgagcacca gaagtgtgag aagacctacc caggaacat 650
 cacagacacc atggtgtgtg ccagcgtgca ggaagguggc aaggactcct 700
 gccagggtga ctccggggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggcacaga tccctgtgtg atcacccgaa agcctgtgtg 800
 ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggacccacc caccacagcc catcacctc catttccact 900
 tgggtgtttgg ttctgttca ctctgttaat aagaaacct aagccaagac 950
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
 tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
 1 5 10 15
 Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
 20 25 30
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
 35 40 45
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50 55 60
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 65 70 75
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
 80 85 90
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 95 100 105

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

gggtggggga ctggaagtcg tgggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

tttttggtct gtaaccag 18

<210> 174

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

tttttgatgt tgcgggggta ggcg 24

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

tggtgtagaca ccaggctttc ggggtg 25

<210> 176

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

cccttgatga tcttggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 177

agggcatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtggt ctgctggagc cgatgcacaa aaccatgcat ttctttattca 50
gattcattgt ttttttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaagagg agagcaccga agaagtgaag atagaagttt tgcctcgtcc 150
agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaatgaag gccaccccaa atgggttggt cttgggtgtg ggcaagtcac 300
aaaaggccta gacattgcta tgacagatat gtgccttgga gaaaagcgaa 350
aagtagttat accccttca ttgcatagc gaaaggaagg ctatgcagaa 400
ggcaagatto caccggatgc tacattgatt ttgagattg aactttatgc 450
tgtgacaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatac aggatgcagt 600
tttgaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
attctacttt ttttttttta gctatttact gtactttatg tataaaacaa 750
agtcactttt ctccaagttg tatttgctat tttcccta tgagaagata 800
tttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850
ttgaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	
				20					25					30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	
				35					40					45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	
				50					55					60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	
				65					70					75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	
				80					85					90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	
				95					100					105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	
				110					115					120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	
				125					130					135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	
				140					145					150	
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	
				155					160					165	
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	
				170					175					180	
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	
				185					190					195	
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	
				200					205					210	
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				
				215					220						

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgtttctgt ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 183
cccttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
gaagtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcacctgat atgacttgta acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<403> Synthetic oligonucleotide probe

<403> 187

ggccattatg agggctacct ggctaaagac ggctggaaat totactgag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg atttctccag gactctgctt totgctgagc 50

ctctttggag ctgtgactca gaaaacccaa acttctctgtg ctaagtgcgc 100

cccaaatgct tctgtgtgca ataacactca ctgcacctgc aacctggat 150

atatctctgg atctgggcag aaactattca cattccccctt ggagacatgt 200

aaagccaggc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250

aagccagggt gatcacctga ggccaggagt ttgagaccag cctggccaac 300

atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcctgac tgcaatccca gttactcggg aggcctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga accagatcc tgcattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttctgttttc atttcggac tgcctctca gtgtttctg ggatccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5				10						15

Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20				25						30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35				40						45

Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50				55						60

Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
				65				70					

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
agggacatt tttttttcca ggc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
tctttgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atcccttgg tgacctcaa agagaagcag agagggcaga 50
ggtaggggggc acagggaaag ggtgacctct gagattcccc tttccccca 100
gaatttggaa gtgaccacac atgggggtca gcatttttt gctctgtgt 150
gttcttgggc taagccagga agccacacag aagattttca atggcactga 200
gtgtgggggt aactcacaga cgtggcaggt ggggctgttt gagggcacca 250
gctgoggtg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gtcactgca ggggcagcag gtactgggtg cgcctggggg aacacagcct 350
cagccagctc gaatggacag agcagatcag gcacagcggc ttctctgtga 400
cccatcaggg ctactggga gctcagcga gctcagcga cgaactcagg 450

atgttgogggg tgggactggc agtccgggta accagtaggg ttcaacccct 500
 ggccttgccc aatgactgtg caaccgtggg caccgagtgc caggtctcag 550
 gctgggggcac caccacccac ccacgggaacc cattcccgga tctgtctcag 600
 tgcctcaaac tctccatagt ctcccatgac acctgacatg gtgtgtatcc 650
 cgggagaatc accagcaaca tgggtgtgtg agggggcgtc cgggggcagg 700
 atgcctgcca ggggtgattct gggggccccc tgggtgtgtg gggagtccct 750
 caaggtctgg tgtcctgggg gtctgtgggg cctgtggac aagatggcat 800
 cctgggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctct ccatcacttc 950
 cctagctcc actcttggtg gcctgggaac ttcttggaac tttaactct 1000
 gccagccctt ctaagaacca cgaggggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr
				125					130					135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His
				140					145					150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser
				155					160					165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile
				170					175					180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala
				185					190					195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu
				200					205					210
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp
				215					220					225
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp
				230					235					240
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn							
				245										

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 ggagccacac gaagctagcc ggagcccgga ccaggcgccct gtgcctctctc 50
 ctgctcctctc gcgcgctccg cgaagcctgg agccggcggg agcccccggc 100
 togcctatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgctc 150
 ggcttgctca aagcccgcca ggagaggagg ctggcccgaga tcaacccggga 200
 gttctctgtg gaccagaagt acagtgatga agagaacott ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagacccac ctggagatga agaagatgat ctacagaggtg acaggagggg 400
 tcagtgcac tatatctac cgagactttg tgaacatgat gctggggaaa 450
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 gacagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgcctgagg accccgctg gactcccgag ccttccacac ccatacctc 600

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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

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				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
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Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
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<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
 20 25 30

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

	35		40		45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro	50		55		60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg	65		70		75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu	80		85		90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe	95		100		105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys	110		115		120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu	125		130		135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg	140		145		150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp	155		160		165
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170		175		180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185		190		195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200		205		210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215		220		225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230		235		240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245		250		255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260		265		270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275		280		285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290		295		300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305		310		315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr					

	320		325		330
Lys Lys Leu Lys Arg Ile Asp Ile Ser	335	Lys Asn Gln Ile Ser Asp	340		345
Ile Ala Pro Asp Ala Phe Gln Gly Leu	350	Lys Ser Leu Thr Ser Leu	355		360
Val Leu Tyr Gly Asn Lys Ile Thr Glu	365	Ile Ala Lys Gly Leu Phe	370		375
Asp Gly Leu Val Ser Leu Gln Leu Leu	380	Leu Leu Asn Ala Asn Lys	385		390
Ile Asn Cys Leu Arg Val Asn Thr Phe	395	Gln Asp Leu Gln Asn Leu	400		405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys	410	Leu Gln Thr Ile Ser Lys	415		420
Gly Leu Phe Ala Pro Leu Gln Ser Ile	425	Gln Thr Leu His Leu Ala	430		435
Gln Asn Pro Phe Val Cys Asp Cys His	440	Leu Lys Trp Leu Ala Asp	445		450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr	455	Ser Gly Ala Arg Cys Ser	460		465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	470	Ile Ser Gln Ile Lys Ser	475		480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	485	Asp Tyr Arg Ser Arg Phe	490		495
Ser Ser Glu Cys Phe Met Asp Leu Val	500	Cys Pro Glu Lys Cys Arg	505		510
Cys Glu Gly Thr Ile Val Asp Cys Ser	515	Asn Gln Lys Leu Val Arg	520		525
Ile Pro Ser His Leu Pro Glu Tyr Val	530	Thr Asp Leu Arg Leu Asn	535		540
Asp Asn Glu Val Ser Val Leu Glu Ala	545	Thr Gly Ile Phe Lys Lys	550		555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	560	Ser Asn Asn Lys Ile Lys	565		570
Glu Val Arg Glu Gly Ala Phe Asp Gly	575	Ala Ala Ser Val Gln Glu	580		585
Leu Met Leu Thr Gly Asn Gln Leu Glu	590	Thr Val His Gly Arg Val	595		600
Phe Arg Gly Leu Ser Gly Leu Lys Thr		Leu Met Leu Arg Ser Asn			

	605		610		615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser	620		625		630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr	635		640		645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu	650		655		660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly	665		670		675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys	680		685		690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala	695		700		705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln	710		715		720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val	725		730		735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met	740		745		750
Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755		760		765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770		775		780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785		790		795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800		805		810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815		820		825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830		835		840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845		850		855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860		865		870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875		880		885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr					

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala		
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr		
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr		
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile		
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser		
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly		
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys		
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys		
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile		
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys		
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

	1460	1465	1470
Ser	Lys	Val	Pro
Met	Glu	Cys	Arg
Gly	Gly	Cys	Gly
Pro	Gln		
	1475	1480	1485
Cys	Cys	Gln	Pro
Thr	Arg	Ser	Lys
Arg	Arg	Lys	Tyr
Val	Phe	Gln	
	1490	1495	1500
Cys	Thr	Asp	Gly
Ser	Ser	Phe	Val
Glu	Glu	Val	Glu
Arg	His	Leu	
	1505	1510	1515
Glu	Cys	Gly	Cys
Leu	Ala	Cys	Ser
	1520		

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 <111> 14
 <112> DNA
 <113> Artificial Sequence

<120>
 <123> Synthetic oligonucleotide probe

<400> 199
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<110> 200
 <111> 14
 <112> DNA
 <113> Artificial Sequence

<120>
 <123> Synthetic oligonucleotide probe

<400> 200
 ttgttgccat tgaggaggag cagc 24

<110> 201
 <111> 50
 <112> DNA
 <113> Artificial Sequence

<120>
 <123> Synthetic oligonucleotide probe

<400> 201
 gaggggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

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 <111> 753
 <112> DNA
 <113> Homo sapiens

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gaatctgctt tttcagttct gtctcgggca ggctttgagg atgaaggctg 150
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 caattactgg ggttcagcc ttggaaaactg gatctgcatg gcattattatg 300
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 caaggaatga actattggca aggcctggaag aaacattgtg agggcagaga 550
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 gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
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 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 131 136

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 146

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

ggcagctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcttggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtgaggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgcacca aggtgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<213> Synthetic oligonucleotide probe

<410> 208

ctactactgt tgcacactgg caaaaatatt ctgaggggtt ggcttgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<410> 209

caggccattt gcacccact gtcttctgtt tcggagccag gccacacgt 50

cctcagcagt gtcattgttt aaaaacgcc aactgaatat atcatgcccc 100

tattaaaaat tgtacatggc tccccattgg tttttggaga aaagttcaag 150

ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200

ggggaagaag atctatcttt actgtcactt ccagatctg cttctcacca 250

agagagattc tttctttaa cgaactatca gggccccaat tgactggata 300

gaggaatata ccacaggaat ggcagaactg atcttagtca acagccagtt 350

cacagctgtt gtttttaagg aaacattcaa gtccctgtct cacatagacc 400

ctgatgtctt ctatccatct ctaaatgtca ccagctttga ctcaagttgt 450

cctgaaaagg tggatgaact agtccccaag gggaaaaaat cctgtgtgtt 500

ctccatcaac agatacgaac ggaagaaaaa ttctgacttg gcaatggag 550

ccctagtaca gctgcttggc agattgacat cccaagattg ggagagggtt 600

catctgatcg tggcaggttg ttatgacgag agagtcttgg agaattgtga 650

acattatcag gaattgaaga aaatgggtca acagtccgac cttggccagt 700

atgtgacctt cttgaggtct ttctcagaca aacagaaaaa ctccctcttc 750

cacagctgca cgtgtgtgtt ttacacacca agcaatgagc actttggcat 800

tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850

cgggttgacc cttggagtc attgacacca gtgtcacagg gtttctgtgt 900

gagcctgacc cgggtgcact ctacagaaga atagaaaagt tcatccgtga 950

accttcttta aaagccacca tgggcctggc tgggaagagc agagtgaagg 1000

aaaaattttt ccttgaagca ttacagaaac agctctaccg atatgttacc 1050

aaactgtctg tataatcaga ttgtttttta gatctccatt aatgtcattt 1100

ttatggattg tagacccagt ttgaaacca aaaaagaaac ctagaatcta 1150

atgcagaaga gatctttttaa aaaataaaact tgagttcttga atgtgagoca 1200
 cttctctata taccacacct cctgttccac ttttcagaaa aacatgtct 1250
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 tgcattcca tgttcagcag agtattttaa ctatattttc tgggattat 1350
 tgcctctctg tatataaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaagtt gattaattg gtttcatagt 1450
 ataattgagag cagggctatt gtatgtccca gattcaatcc accgaagtgt 1500
 tcactgtcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550
 catagcgaga gtgcctctga ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaaagggt gtttatcata aaaaaaaaaa aaaaaaaaa 1643

4210: 210
 4211: 323
 4212: FRT
 4213: Homo sapiens

4400: 210
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
 1 5 10 15
 Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
 20 25 30
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
 35 40 45
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
 50 55 60
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
 65 70 75
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
 80 85 90
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
 95 100 105
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
 110 115 120
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
 125 130 135
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
 140 145 150
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

155	160	165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg		
170	175	180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val		
185	190	195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe		
200	205	210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val		
215	220	225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu		
230	235	240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly		
245	250	255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu		
260	265	270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg		
275	280	285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg		
290	295	300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr		
305	310	315
Arg Tyr Val Thr Lys Leu Leu Val		
320		

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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cttcgggata ttgcgcgtta ccttcttctg ggcgttggtg ggagccgtgc 100

tctacctata tcgggtctcc agacaagctg caggaattcc agggattact 150

ccaactgaag aaaaagatgg taattctcca gatattgtga atagtgggaag 200

tttgcattgag ttccctggta atttgcattg gagatatggg cctgtggtct 250

ccttctgggt ttgcaggcgc ctgcgttgta gtttgggcac tgttgatgta 300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350

gctgaagtca ttattaaggt atcaattctg tggtaggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg cctctctctt aaagctttca gaagaattat tagataaatg 500
 gtctctctac ccagagaccc agcaagtgc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg ctccagaaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcacc atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cactctgaa gaagtccaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tctgttact ccagagaaaa 1000
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaacgattt attattccta gagagacct cgtcctttat gcccttggtg 1150
 tggtaactta ggatcctaact acttggtcat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct caattggatt 1250
 ctccaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggtac actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala			
				20					25					30			
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu			
				35					40					45			
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn			
				50					55					60			
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg			
				65					70					75			
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His			
				80					85					90			
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys			
				95					100					105			
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn			
				110					115					120			
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu			
				125					130					135			
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu			
				140					145					150			
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser			
				155					160					165			
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val			
				170					175					180			
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln			
				185					190					195			
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu			
				200					205					210			
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu			
				215					220					225			
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys			
				230					235					240			
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser			
				245					250					255			
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser			
				260					265					270			
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys			
				275					280					285			
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys			
				290					295					300			

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	305	310	315
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	320	325	330
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	335	340	345
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	350	355	360
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	365	370	375
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	380	385	390
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	395	400	405
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	410	415	420
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	425	430	435
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	440	445	450
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				455	460	

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctatgatttgt cgggttgagg ggagacttca ggagtgcgtg tctctgaact 50
 tccagctca gagacggcgg ccttgtccc caggggcat gggccgggtc 100
 tcagggttg tgcctctcg ctctcgacg ctctggcgc atctggtggt 150
 cgtcaccacc ttattctggt ccggggacag caacatacag gctgcctgc 200
 ctctcaggtt caccocagag gagtatgaca agcaggacat tcagctggtg 250
 gcggcgtct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcacc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtga ctaggtattg gtacatttt gtctcttga gtgccttcc 450

agctgtcaact gaaatgggtt tatctgtcac cgtctttggg ctgaaaaaga 500
 aacctttctg attaccttca tgaagggaac ctaaggacga agctacagg 550
 ggaaggggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600
 ttccctcggg aaactgcttc tgcctggagga tatgtgttgg aataattacg 650
 tcttgagctt gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tcttttctag taacattaag acttatatac agttttaggg gacaattaaa 750
 aaaaaaaaaa 759

<210> 214
 <211> 140
 <212> FRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
 tccgggaccc tgcggccctg ccactatgtc ccggcgctct atgctgcttg 50

cctgggctct ccccagctc cttcgactcg gaggggctca ggagacagaa 100
 gacccgggct gctgcagccc catagtgcgc cggaaacagt ggaaggccct 150
 ggcacacagag tgcgcccagc acctgagcct gcccttacgc tatgttggtgg 200
 tatgcacac ggcgggcagc agctgcaaca ccccagctc gtgcacagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtgga 300
 cgtgggctac aacttctga ttggagaaga cgggctcgta tacgagggcc 350
 gtgactggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcac gggcaactac atggatcggg tgcacacac 450
 ccaggccatc cgggcagccc agggctctact ggcctgcggg gtggctcagg 500
 gagcctgag gtccaaactat gtgtcaaaag gacaccggga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctacggctcc cctgagggcc ctgctgctcc gcaccccatc cctccctcc 650
 catggccaaa aacccactg tctctctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1				5					10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
			20						25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
				35					40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
				50					55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
				65					70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
				80					85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
				95					100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
				110					115					120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
			125						130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
			140						145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
			155						160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
			170						175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
			185						190					195

Pro

<210> 217
 <211> 1871
 <212> DNA
 <213> Homo sapiens

<400> 217
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 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
 tctatctggt catctgtggc caggatgatg gtctctccgg ctacagaggac 150
 cctgagcgtg atgaccaaga gggccagccc cggcccgggg tgctctggaa 200
 ggjgggcac atctcaccta agtcccggcc catggccaat tccactctcc 250
 tagggctgct ggcccggcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaacggc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350
 ctttggtgg ggagacttct actccaaat caagacgggt gcctgaacc 400
 tggctgtcac agggaagatt gtggaccatg gcaatgggac ctccagcgtc 450
 cacttccaa acaatgcac aggcagggga aacatctcca tcagcctcgt 500
 gcccccagc aaagctgtag agttccacca ggaacagcag atcttcacgc 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtj ggagaaggta 600
 gaaagggggc gcgggacctc gctttgcacc cagcaccag ccaagatctg 650
 ctcccgagac cagctccaga gctcagccac ctggagctgc tcccagccct 700
 tcaagctcgt ctgtgtctac atgccttct acagcagga ctatcggctg 750
 gtccagaagg tgtgcacaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaacgggg caggccacag aggcagggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacacccgg cagggaaggg 900
 gttgggcctc aggcagggag ggggtggag acgaggagat gccaaagtgg 950
 gccagggcca agtctcaagt ggcagagaaa ggytcccaag tgcctggccc 1000
 aacctgaagc tctggagtga ctagatcaca ggagcactgg aggaggagtg 1050
 ggtctctctg gcagctcac aggtcttga caggaccca cagagagatg 1100
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcatgggag gaagctaagc ccttggttct tgcctcctg aggaaagata 1200
 gcaacagggg ggjggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
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 gccagaggag ctctccagcc ctgcctagtg ggcgccctga gcccttgtc 1350
 gtgtgtgag catggcatga ggctgaagtg gcaacctgg ggtctttgat 1400
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
 ttcctcttc tgcagtact cccctgtac caaccattgc tgatggcaca 1500
 cccatcotta agctaagaca ggaagattgt ggtctccca cactaaggcc 1550
 acagcccata cgggtgctgt gtgtccctct tccacccaa cccctgctgg 1600
 ctctctctgg agcatccatg tccggagag ggtccctca acagtcagcc 1650
 tcaactgtca gacgggggtt ctccggatc tggatggggc cggcctctca 1700
 gcaacgggca cgggtggggc ggggcggggc cgcagagcat gtgtgggatc 1750
 tgtctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
 aacgtgtgat tctgaacttt tgtgtgaaga atcgtgttct tggagcagga 1850
 aataaagctt gccccggggc a 1871

<210> 218
 <211> 252
 <212> FRT
 <213> Homo sapiens

<400> 218
 Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
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 Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
 20 25 30
 Gln Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	215	220	225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	230	235	240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				245	250	

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 <213> Homo sapiens

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 agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gagcgcgcgc gcgcgtcgct cctgcagcgc tctcgaccta gcgcctagca 250
tcttcgcgag caccgggata cgggggtagg aggcgaagcg ggagagcacc 300
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 ttcaaatac ccatatctaa atttagtga atatcttgtc ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

02100 220
 02110 201
 02120 PRT
 02130 Homo sapiens

04000 220
 Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
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 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
 20 25 30
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
 35 40 45
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
 50 55 60
 Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
 65 70 75
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
 140 145 150
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
185 190 195

Phe Leu Val Phe Pro Leu
200

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<220>
<223> Synthetic oligonucleotide probe

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<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
aggaagagga gcccttggag tcgg 24

<210> 223
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

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tatcatcttc ctcatgcgg gagctttctt ctggttgggtg tctctactga 150
tttcgtccct tggttggttc atggcaagag tcattattga caacaaagat 200

gaacaaacac agaaatatct gctgatcttt ggagagcttg tctctgtcta 250
 tatccaagaa atgttcagat ttgcatatta taaactotta aaaaaagcca 300
 gtgaaggctt gaagagtata aaccacaggtg agacagcacc ctctatgoga 350
 ctgctggcct atgtttctgg ctggggcttt ggaatcatga gtggagtatt 400
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 gtcatttat tcttgcctgt attctggggc attgtatttt ttgatggctg 550
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<210> 325
 <211> 357
 <212> PRT
 <213> Homo sapiens

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 Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
 35 40 45
 Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
 50 55 60
 Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
 65 70 75
 Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
 80 85 90
 Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
 95 100 105

Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

42100 226
 42110 3939
 42120 DNA
 42130 Homo sapiens

44000 226
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 gagccatctg ggggtttctg ggcccaagaa cgtctgcag aaagacgccg 150
 agtttgagcg caactacgtg gacgaggtca acagcgagct ggtcaacatc 200
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 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 217
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 Val Gln Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
 20 25 30
 Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser

	125		130		135
Thr Leu Ser Pro	Val Asn Thr Thr Tyr	Gln Leu Arg Val Ser Arg			
	140		145		150
Met Asp Asp Phe	Val Leu Arg Thr Gly	Glu Gln Phe Ser Phe Asn			
	155		160		165
Thr Thr Ala Ala	Gln Pro Gln Tyr Phe	Lys Tyr Glu Phe Pro Glu			
	170		175		180
Gly Val Asp Ser	Val Ile Val Lys Val	Thr Ser Asn Lys Ala Phe			
	185		190		195
Pro Cys Ser Val	Ile Ser Ile Gln Asp	Val Leu Cys Pro Val Tyr			
	200		205		210
Asp Leu Asp Asn	Asn Val Ala Phe Ile	Gly Met Tyr Gln Thr Met			
	215		220		225
Thr Lys Lys Ala	Ala Ile Thr Val Gln	Arg Lys Asp Phe Pro Ser			
	230		235		240
Asn Ser Phe Tyr	Val Val Val Val Val	Lys Thr Glu Asp Gln Ala			
	245		250		255
Cys Gly Gly Ser	Leu Pro Phe Tyr Pro	Phe Ala Glu Asp Glu Pro			
	260		265		270
Val Asp Gln Gly	His Arg Gln Lys Thr	Leu Ser Val Leu Val Ser			
	275		280		285
Gln Ala Val Thr	Ser Glu Ala Tyr Val	Ser Gly Met Leu Phe Cys			
	290		295		300
Leu Gly Ile Phe	Leu Ser Phe Tyr Leu	Leu Thr Val Leu Leu Ala			
	305		310		315
Cys Trp Glu Asn	Trp Arg Gln Lys Lys	Lys Thr Leu Leu Val Ala			
	320		325		330
Ile Asp Arg Ala	Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala			
	335		340		345
Asp Ser Phe Pro	Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly			
	350		355		360
Ser Phe Glu Asn	Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser			
	365		370		375
Ala Gly Thr Gly	Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe			
	380		385		390
Glu Pro Val Gly	Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val			
	395		400		405
Glu Glu Asp Asp	Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys			

410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala		
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe		
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val		
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn		
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly		
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile		
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile		
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu		
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr		
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys		
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met		
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro		
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile		
605	610	615
Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn		
620	625	630
Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr		
635	640	645
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu		
650	655	660
Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp		
665	670	675
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val		
680	685	690
Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr		

695	700	705
Gly Leu Ile Met Arg Pro Asn Asp Phe	Ala Ser Tyr Leu Leu Ala	
710	715	720
Ile Gly Ile Cys Asn Leu Leu Leu Tyr	Phe Ala Phe Tyr Ile Ile	
725	730	735
Met Lys Leu Arg Ser Gly Glu Arg Ile	Lys Leu Ile Pro Leu Leu	
740	745	750
Cys Ile Val Cys Thr Ser Val Val Trp	Gly Phe Ala Leu Phe Phe	
755	760	765
Phe Phe Gln Gly Leu Ser Thr Trp Gln	Lys Thr Pro Ala Glu Ser	
770	775	780
Arg Glu His Asn Arg Asp Cys Ile Leu	Leu Asp Phe Phe Asp Asp	
785	790	795
His Asp Ile Trp His Phe Leu Ser Ser	Ile Ala Met Phe Gly Ser	
800	805	810
Phe Leu Val Leu Leu Thr Leu Asp Asp	Asp Leu Asp Thr Val Gln	
815	820	825
Arg Asp Lys Ile Tyr Val Phe		
830		

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 <211> 2848
 <212> DNA
 <213> Homo sapiens

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 ttgggcgctg gagggcctgt cctgaaccatg gtccttgcct ggctgtggct 150
 gctttgtgtc tccttccccc aggtctctcc caaggccag cctgcagagc 200
 tgtctgtgga agttccagaa aactatgggtg gaaatttccc ttataacctg 250
 accaagttgc cgtgtccccc tgagggggct gaaggccaga tcgtgctgtc 300
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<211> 807

<212> PRT

<213> Homo sapiens

<400> 219

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			20					25				30		

Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
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Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
			50					55				60		

Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
			65					70				75		

Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80										85					90				
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

	365		370		375
Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala	380		385		390
Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu	395		400		405
Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met	410		415		420
Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val	425		430		435
Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile	440		445		450
Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro	455		460		465
Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu	470		475		480
Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr	485		490		495
Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val	500		505		510
Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser	515		520		525
His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly	530		535		540
Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val	545		550		555
Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu	560		565		570
Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr	575		580		585
Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu	590		595		600
Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly	605		610		615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp	620		625		630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu	635		640		645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His					

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Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
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Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		
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<110> 230

<111> 50

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 230

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<110> 231

<111> 24

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 231

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<110> 232

<111> 13

<112> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

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<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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 <211> 421
 <212> FRT
 <213> Homo sapiens

<400> 234
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 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165
 Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
 170 175 180
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
 185 190 195

Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	
				200					205					210	
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	
				215					220					225	
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
				230					235					240	
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	
				245					250					255	
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	
				260					265					270	
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	
				275					280					285	
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	
				290					295					300	
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	
				305					310					315	
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
				320					325					330	
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
				335					340					345	
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	
				350					355					360	
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
				365					370					375	
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
				380					385					390	
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
				395					400					405	
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	
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Tyr

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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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 aacacgcact ttgccttccg cctataccgc aggcctggttt tggagacccc 250
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 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
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 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
 200 205 210

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggcacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<410> 238

ctttgctggtt ggcatatgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactggggg totccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggatataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

agcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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agctgcccac gctgagtc aaagattotte ccaggaacac aaacgtagga 100

gacccacggt cctggaagca ccagccttta totcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgcctt cttaaagtctt ggtacatcta 200

ggaccacaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttgggtta ctattgact tagaagctgc 300
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 gatgaactca gttataggag aaaacctcca tgcctggactc catctggcat 2350
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	
Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80				85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95				100					105	

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
110 115 120

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
125 130 135

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
140 145 150

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
155 160 165

Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
170 175 180

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
185 190 195

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
200 205 210

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
215 220 225

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
230 235 240

Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
245 250 255

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
260 265 270

Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
275 280 285

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
290 295 300

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
305 310 315

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
320 325 330

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
335 340 345

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
350 355 360

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
365 370 375

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
380 385 390

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				395					400					405
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				410					415					420
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala
				425					430					435
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				440					445					450
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				455					460					465
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala
				470					475					480
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala
				485					490					495
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile
				500					505					510
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe
				515					520					525
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn
				530					535					540
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly
				545					550					555
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro
				560					565					570
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile
				575					580					585
Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro				
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<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggtgtgga taga 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggacccagga atottgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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cccatatgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
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<210> 248
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 248
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 20 25 30
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
 110 115 120
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
 170 175 180
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
 185 190 195
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
 200 205 210
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 250
 aagttctct ctttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 tgaacccatt gagaaggcca ttgaagggat caaccgaggg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252
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 gggggggacc gggggggcga gctgcggccc gtgagtcggg ccgagccacc 200
 tgagcccgag ccgcggggaa ccgtcgctcc tgcctccga atgctggcca 250

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile	125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly	140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn	155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp	170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala	185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe	200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro	215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe	230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly	245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu	260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile	275	280	285
Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp	290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp	305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro	320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr	335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val	350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys	365	370	375
Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
				710					715					720	
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
				725					730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
				740					745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
				755					760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
				770					775					780	
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
				785					790					795	
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
				800					805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val				
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 254
 agcccggtgca gaatctgttc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 tgaagccagg gcagcgtcct ctgg 24

<210> 256
 <211> 18
 <212> DNA
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<220>

<223> Synthetic oligonucleotide probe

<400> 256

gtatagggtg cagttggc 18

<210> 257

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 258

gagtgacaga tttttctatc gggacagccc gtgcagaatc tgctc 45

<210> 259

<211> 4563

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 3635

<223> unknown base

<400> 259

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agggcgggac gggagcccgg actcgtctgc cgcgcgcgtc gtgcgcgtcg 150

tgccggcccc ggcgcccgcc ggcgcagcgg gaggagccgc cgcacactcg 200

cgcgcgagcc gccgctagcg cgcgcgcggc atggtcacct cttaaaggcg 250

caggcccggg cggcgggggc ggggtgtcgg aacaaagcgc cggcgcgggg 300

actgcggggg gctcgggggc cgcgatgggc ggcgcgggac cgcggcgggc 350

gggcgcgtgc cggggccggg cctcgcggcg ctaggcgggg ctggcctccg 400

tgggcggggg cagcgggctg aggggcggcg gaggcctggg cggcggcggc 450

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tggatgcaca agagtgggc aagagaatca atcaggaatc tggatccttg 2000
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<210> 260

<211> 802

<212> FRT

<213> Homo sapiens

<410> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg
				20					25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val
				245					250					255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser
				260					265					270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys

	275		280		285
Lys Gly Tyr Ile Arg Asp Leu His Asn Ser	290	Lys Ile His Gln Ala	300		
Ile Thr Leu His Pro Asn Lys Asn Pro	305	Pro Tyr Gln Tyr Arg Leu	315		
His Ser Tyr Met Leu Ser Arg Lys Ile Ser	320	Glu Leu Arg His Arg	330		
Thr Ile Gln Leu His Arg Glu Ile Val	335	Leu Met Ser Lys Tyr Ser	345		
Asn Thr Glu Ile His Lys Glu Asp Leu Gln	350	Leu Gly Ile Pro Pro	360		
Ser Phe Met Arg Phe Gln Pro Arg Gln Arg	365	Glu Glu Ile Leu Glu	375		
Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr	380	Ser Ala Val Asp Gly	390		
Gln Pro Pro Arg Arg Gly Met Asp Ser Ala	395	Gln Arg Glu Ala Leu	405		
Asp Asp Ile Val Met Gln Val Met Glu Met	410	Ile Asn Ala Asn Ala	420		
Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys	425	Glu Ile Gln Tyr Gly	435		
Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala	440	Glu Tyr Ile Leu Asp	450		
Leu Leu Leu Leu Tyr Lys Lys His Lys Gly	455	Lys Lys Met Thr Val	465		
Pro Val Arg Arg His Ala Tyr Leu Gln Gln	470	Thr Phe Ser Lys Ile	480		
Gln Phe Val Glu His Glu Glu Leu Asp Ala	485	Gln Glu Leu Ala Lys	495		
Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser	500	Phe Leu Ser Asn Ser	510		
Leu Lys Lys Leu Val Pro Phe Gln Leu Pro	515	Gly Ser Lys Ser Glu	525		
His Lys Glu Pro Lys Asp Lys Lys Ile Asn	530	Ile Leu Ile Pro Leu	540		
Ser Gly Arg Phe Asp Met Phe Val Arg Phe	545	Met Gly Asn Phe Glu	555		
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val		Lys Leu Val Val Leu			

560										565					570				
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu					
				575					580					585					
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
				590					595					600					
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
				605					610					615					
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
				620					625					630					
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
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Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
				680					685					690					
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
				695					700					705					
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
				710					715					720					
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725					730					735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740					745					750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755					760					765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
				770					775					780					
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
				785					790					795					
Asn	Gly	Ser	Val	Arg	Thr	Ala													
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<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

gtgcacactac ggggtgtgga cgac 24

<210> 262

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

tcccatttct tccgtggtgc ccag 24

<210> 263

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 263

ccagaagaag tcttccatga tgcacaagta catgcacgac cactac 46

<210> 264

<211> 1419

<212> DNA

<213> Homo sapiens

<400> 264

ggacaaacgt tgcctgggtgt cccagggcct gaggcaggac ggtactccgc 50

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gttccggctg catggcagag tgcacaggac gacgcctatg aagcccttag 150

tctttctagt tgcgcttttg ctatggcctt cgtctgtgac ggcttatccg 200

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<210> 265
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 265
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 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
 35 40 45
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser
 50 55 60
 Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys
 65 70 75
 Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu
 80 85 90

Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	
				95						100				105	
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	
				110					115					120	
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	
				125					130					135	
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	
				140					145					150	
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	
				155					160					165	
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	
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Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	
				185					190					195	
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	
				200					205					210	
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	
				215					220					225	
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	
				230					235					240	
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	
				245					250					255	
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	
				260					265					270	
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	
				275					280					285	
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	
				290					295					300	
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	
				305					310					315	
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	
				320					325					330	
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	
				335					340					345	
Leu	Leu	Lys	Val	Tyr											
				350											

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<411> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Thr Ser Ala Glu	Ala Met Glu Val Arg Phe	Phe Arg Asn Gln Phe			
	50	55			60
His Ala Val Val	His Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser			
	65	70			75
Lys Gln Met Pro	Gln Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp			
	80	85			90
Ser Ile Ala Gly	Gly Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr			
	95	100			105
Pro Ser Asp Ile	Gly Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile			
	110	115			120
Tyr Asp Glu Glu	Ala Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly			
	125	130			135
Ser Leu Pro Leu	Ile Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile			
	140	145			150
Gln Leu Leu Cys	Leu Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala			
	155	160			165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg			
	170	175			180
Ala Asn Ala Asp	Gly Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile			
	185	190			195
Ile Val Gln Glu	Asn Ala Gly Ser Ile Leu	Cys Ser Ile His Leu			
	200	205			210
Ala Glu Gln Ser	His Glu Val Glu Ser Lys	Val Leu Ile Gly Glu			
	215	220			225
Thr Phe Phe Gln	Pro Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu			
	230	235			240
Gly Leu Leu Cys	Gly Ala Leu Cys Gly Val	Val Met Gly Met Ile			
	245	250			255
Ile Val Phe Phe	Lys Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp			
	260	265			270
Trp Arg Arg Lys	His Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys			
	275	280			285
His Ala Val Glu	Val Thr Leu Asp Pro Glu	Thr Ala His Pro Lys			
	290	295			300
Leu Cys Val Ser	Asp Leu Lys Thr Val Thr	His Arg Lys Ala Pro			
	305	310			315
Gln Glu Val Pro	His Ser Glu Lys Arg Phe	Thr Arg Lys Ser Val			

	320		325		330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val					
	335		340		345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp					
	350		355		360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn					
	365		370		375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr					
	380		385		390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr					
	395		400		405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe					
	410		415		420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys					
	425		430		435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr					
	440		445		450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp					
	455		460		465

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<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 gtcattctca tatccctgat tgcctggga gtgtgcattg gactcactgt 150
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 tgtcatttac aactgacaaa ctatatgtgt agtttggcag agaggcttct 250
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 caaacttcat gcaatgtact tgttctaaga aaattaaaga aaatatattat 2050
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<210> 269
 <211> 423
 <212> PFT
 <213> Hcno sapiens

<400> 269
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210

Trp Asp Gly Ser	His Arg Cys Gly Ala Thr	Leu Ile Asn Ala Thr
215	220	225
Trp Leu Val Ser	Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro	
230	235	240
Ala Arg Trp Thr	Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys	
245	250	255
Met Lys Arg Gly	Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys	
260	265	270
His Pro Ser His	Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser	
275	280	285
Pro Val Pro Tyr	Thr Asn Ala Val His Arg Val Cys Leu Pro Asp	
290	295	300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly	
305	310	315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg	
320	325	330
Gln Ala Gln Val	Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro	
335	340	345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly	
350	355	360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly	
365	370	375
Pro Leu Val Ser	Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly	
380	385	390
Ile Val Ser Trp	Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly	
395	400	405
Val Tyr Thr Arg	Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys	
410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
			20					25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40						45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	
				57					55					60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	
				65					70					75	
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

0210> 272

0211> 2397

0212> DNA

0213> Homo sapiens

0400> 272

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<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273
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 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	170	175	180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	185	190	195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	200	205	210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	215	220	225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	230	235	240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	245	250	255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	260	265	270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	275	280	285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	290	295	300
Glu	Met	Glu	Glu	Leu											305		

<210> 274

<211> 2963

<212> DNA

<213> Homo sapiens

<400> 274

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ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150

cttggggtga caatctcagc tccaggtac agggagaccg ggaggatcac 200

agagccagca tgttacagga tctgacagt gatcaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aacccgttat ccccatggag accttcagaa 300

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<210> 275
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 275
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 Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
 35 40 45
 Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
 50 55 60
 Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
 65 70 75
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
 80 85 90
 His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
 95 100 105
 Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
 110 115 120
 Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
 125 130 135
 Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
 140 145 150
 Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
 155 160 165
 Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
 170 175 180

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	185	190	195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	200	205	210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	215	220	225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	230	235	240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	245	250	255
Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	260	265	270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	275	280	285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	290	295	300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	305	310	315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	320	325	330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	335	340	345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	350	355	360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	365	370	375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	380	385	390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	395	400	405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	410	415	420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu				425	430	

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met Arg
200	205	210
Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu Arg
215	220	225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser Thr
230	235	240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
245	250	255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
260	265	270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr Thr
275	280	285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
290	295	300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro
305	310	315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320	325	330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335	340	345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350	355	360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365	370	375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380	385	390
Phe Met Lys Asp	His Phe Leu Met Asp	Gln Gln Val Val Gly Thr
395	400	405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410	415	420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425	430	435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440	445	450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455	460	465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470	475	480

Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala	575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu	590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln	605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly	620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln	635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His	650	655	660
Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala	665	670	675
Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu	680	685	690
Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser	695	700	705
Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu	710	715	720
Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His	725	730	735
Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp	740	745	750
Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala	755	760	

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
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<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggctct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 281
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<212> DNA
<213> Homo sapiens

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gccttggggg ggtctgtttg gtgggggatg tcaccatttc tagggagctt 1700
ccactagtt ctggcagccc cattctctag tcttctagct tatctctgt 1750
ttcttgaag aacaggaaaa atggccaaaa atcatcctt ccacttgcta 1800
atcttgctac aaattcctcc ttaactagct ctgctgcta gcagaaatct 1850

ttccagtcctt cttgttcctcc tttgttttgc atcagcaagg gctatgctgt 1900
 gattctgtct ctgagtgaact tggaccactg acctcagat ttccagcctt 1950
 aaaatccacc ttctttctca tggcctcttc cgaatcacac cctgactctt 2000
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcctctact 2050
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
 ttctgttttg ttctccaca tattctcttc aatgttcagg aagcctgcc 2150
 tgtgcttgag agttcagggc cggacacagg ctccacaggtc tccacattgg 2200
 gtccctgtct ctggtgccca cagtgcgctc cttcttggct gaggaggcat 2250
 ggagactgta ggtttccaga tttcctgaaa aataaaaagt tacagcgta 2300
 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
 Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro
 1 5 10 15
 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu	Phe Gly Leu Pro Ile Pro	
170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser	Leu Leu Thr Asp His Met	
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe	Leu Met Phe Phe Ser Phe	
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser	Thr Phe Asp Asn Thr Ile	
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg	Pro Val Leu Ser His Leu	
230	235	240
Leu Leu Lys Ala Glu Leu Trp Phe Ile	Asn Ser Asp Phe Ala Phe	
245	250	255
Asp Phe Ala Arg Pro Leu Leu Pro Asn	Thr Val Tyr Val Gly Gly	
260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	

	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile Asp His Val Leu Gln Thr				
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp				
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu				
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala				
	500		505		510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr					
	515		520		

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 284
 tcaggttggt ctocaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 285
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50

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gtgtctgtccc atccagcagg gctaccctga agctctgggt gcagccctcc 200
cgctccagtgg gcaggcggtt tcatccctcc tttctctccc aaagcccaac 250
tctgttcact gcatgctctg ccaaggagga gggaaatgca gtgacagpag 300
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc aggggtgcgg cggtgagaat 400
ccaggggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450
gggttgacaga gccctccagc catgtttgga gccaaagcac actggctacc 500
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atgctgaaca ctgggcctgt catctcagcc tttgcacatg atcctgacgt 950
gaccggggag gcagcacca gctctgtgt actgccttg gacctgggg 1000
aacgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
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 caactagaga atggt-ggtca gtgagacact atagaattac taaggagaag 2250
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
 1 5 10 15

Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
 20 25 30

Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45

Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60

Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 238

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

agggcagggcac cagctctgtg ctac 24

<210> 299

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 269

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgtctact ggccttggac cctgggggacc gactgtctct gc 42

<210> 291

<211> 1670

<212> DNA

<213> Homo sapiens

<400> 291

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tagcgcgcaca ggcctgacgc cgtcccgga cccctgtgt ctgcgcgaag 100
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ttcccggggg gcctgactg ggcgggcttc agccatgaag accctcatag 200
ccgcctactc cggggctctg cggggcgagc gtcaggccga ggcctgacgg 250
agccagcgct ctacgggag acctgcgctg tgcgcgcagg ggtctgggag 300
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 aactgtacca caacatgtac atggaggccc tgggtgaagct cttagacaag 1300
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 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
 gaaattataa caattttgt aaacaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
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 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292
 Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
 1 5 10 15
 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
 20 25 30
 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	380	385	

<210> 193

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 193

gctgacctgg ttcccatcta ctcc 24

<210> 194

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aaagaatgaat tgtacaaagc aggtgatatt cgaggagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggggggggg atgggggggg gggggggggg ggggggcaact cgctgaggcc 50

ccagcgcagg gcgggggggg gcccagggcc gaggagcgcg gcggccagag 100

cgggggcgcg gaggcgacgc cgggggagcc cgcgcgacga gcaggtggcg 150

ggggctgcag gottgtccag ccggaagccc tgagggcagc tgttccact 200

ggctctgtcg accttgtgcc ttggacggct gtctcagcg aggggccgtg 250

cccccgtccc tgagcagcgc catggggctg ctggccttcc tgaagacca 300

gttcgtgtcg caactgtcgg tcggctttgt cttcgtggcg agtggctcgg 350

tcataaactt cgtccagctg tgcacgtcgg cgtctcggcc ggtcagcaag 400

cagctctacc gcggcctcaa ctgcgcctc gctactcac totggagcca 450

actggtcatg ctgctggagt ggtggctcct caccgagtg acactgttca 500

cggaaccagg caccgtagag cgttttggga aggagcagc agtcacatc 550

ctcaaccaca aattcgagat cgaattctc tctgggtgga ccattgtgtg 600

gggcttcgga gtgctgggga gctccaaagg cctcgctaag aaggagctgc 650

tctacgtgcc cctcatcggc tggacgtggc actttctgga gattgtgttc 700

tgcaagcgga agtgggagga ggaccgggac accgtggctg aagggtgag 750

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 ccagggagac tgaagtggga ggatgccttg ggcattgagaa gtcgaggttg 3000
 cagttagtcg aggttgtgcg actgcattcc agcctggaca acagagttag 3050
 acctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
			20					25					30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
			35					40					45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
			50					55					60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
			65					70					75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
				350					355					360					
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

cttctctctgt ggggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gccaactcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgcccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgtcttgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100

tgcttttaga ctgggggcact tottgcttat ttctttggta ggaaaggggc 150

tcagtttgtc ttgtgggggt ggtggcaggc aggcgggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagtggggt ctgagacctg ctctctcagt aaaattcctg ggatctgctt 300

atactttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tottaggata aaagtattta gagctacaag agccctcatg 400

gtatggcccc tgccccccctg gccagattca ttgtacatgt ggtgtttctct 450
 ttttgttctct gtaatgtgggt atgcatgggg gtctttgcac aagcttttcc 500
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
 atgtagtcat cctgcagatt tcaattctaa catcatttcc tccagggatc 600
 ctggctgcac agaattctcat ctgttttaat gctctcataa gaccacttgt 650
 ttcctttttg cagcaattgc cactcagttg tatctttatg tgcttttgtg 700
 gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgctg 750
 agggccaagg gcattgtctg gctgcacagg tatagtgcct acatgtgggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtagg ccacagcattg taaattcaca 900
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 gccacaggtg gccatctcta acaaaactccc acgtgatgct gatgctggtc 1000
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 acctggagtc aggatttcaa gactagcttg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgctgtg 1200
 gtcccagcta ctggggaggg tgaagcaaga gaatcgcttg aacctgggag 1250
 ggggaggttg cagtgagecg agatcaggcc actgtattcc aaccaggggtg 1300
 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25					30	
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40					45	
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55					60	
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp

	65	70	75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr			
	80	85	90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln			
	95	100	105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu			
	110	115	120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr			
	125	130	135
Cys Gly Val Leu Leu Ser Phe Leu			
	140		

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 aagggtgctgt gattataggt gtaagccacc gtgtctggcc totgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgtctgtg tggtagtgc tctactcct acctacatta aaatctgttt 200
 ttgtttctct tgtaactage ctttaacctc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaac tgacctcac totggaaaga gaacagaggt 300
 ttctacccac acctccct cgaagccggg gacagcctca ccttctgtgc 350
 ctctcctgtg agcagtgc ccaccaactg tctcagctct ggaggcactg 400
 actcggggcag tgcaggtagc tgagcctctt ggtagctggc gctttcaagg 450
 tgggccttgc cctggcctga gaagggttg acaagccaga agatttcata 500
 ggcgatggct cccactgcc aggcctcagc cttgtctgag tcaatcactg 550
 cctcggggcc aggaaggcc gtggacaact gctcagaagc agtgggtgag 600
 acatcacgtg gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac totgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgt tagaccact ggtttatgtg 750
 acaggacttg cattctctg gaacatgagg gaacgcgga ggaaagcaaa 800
 gtgcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

gtgggggttat cacaaggaat agagtctctt gcattcagtg gacatgtggg 900
 ggaaggggtg ccgatggggc atgacacact cgggactcac ctctgggggc 950
 atcagacagc cgtttccggc ccgatccacg taacagctgc tgaagggcaa 1000
 ctgcaggcgc atgtctctat cagccaggga gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100
 ctccctctct tccctctgag aggcctctct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgg tcagtgttgg ccaggaggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgtgtgtgc aacacggaaa 1250
 tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaa gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaaagg 1350
 agctagagct tggttcaaat gatctccaag ggcccttata cccaggaga 1400
 ctttgatttg aatttgaaa cccaaatcca aacctaaaga ccaggtgcat 1450
 taagaatcag ttattgcggg gtgtgggtgg ctgtaatgcc aacattttgg 1500
 caggccagagg cgggttagat acctgaggtc aggagttcaa gaccagctg 1550
 gccaacatgg tgaacccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattggg gtgtgtgctt gtatccagc tactcgggag gctgagacag 1650
 ggagaattact tgaacctggg aggtgaagga ggtgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctacagaaaa ataaaaaag 1750
 aattatgggt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro

	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
	80		85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305
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 tgtcaactgcc tcccgccgcc tcttgcgcgc gccatgaccc agccgggtgcc 100
 ccggctctcc gtgcgcgcgc cgttggccct gggctccagc gcactgggcg 150
 ccgccttcgc cactggcctc ttctggggga ggccgtgccc cccatggcga 200
 ggccggcgag agcagtgcct gcttccccc gaggaacagc gcctgtggca 250
 gtatcttttg agccgctcca tgggggagca ccgggcgctg cgaagcctga 300
 ggtgtgtgac cctggagcag ccgcaggggg attctatgat gacctggag 350
 caggccacgc tcttggccaa cctggcgagg ctcatccagg ccaagaaggc 400
 gctggacctg ggcaccttca cgggtactc cgccttggcc ctggccttg 450
 cgttgcgcgc ggaagggcgc gtgggtgacct ggcaggtgga ccggcagccc 500
 ccggagctgg gacggccctc gtggaggcag gccgaggcgg agcacaagat 550
 ccacctccgg ctgaagcccg ccttggagac cctggacgag ctgttggcgg 600
 cgggcgaggg ccgcaccttc gacgtggcgc tgggtggatgc ggacaaggag 650
 aactgtctcc ctactacga gcgttgcctg cagctgtctg gaccggagg 700
 cactctgcgc gtctccagag tctgttggcg ccggaagggt ctgcaacctc 750
 ccgaaaggga cgtggcgccc gactgtgtgc gaaacctaaa cgaacgcctc 800
 ccgggggagc tcagggtcta cctcagcctc ctggccttgg gcgatggact 850
 cactttggcc ttcagatct agggctggcc cctagttagt gggctccagg 900
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggagac aaaaaaaaaa aaaaaaaaaa 999

<210> 306
 <211> 262
 <212> PRT
 <213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala	
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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe	
				20					25					30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys	
				35					40					45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser	
				50					55					60	
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
				245					250					255	

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
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gctaagatga agggctaccc tcactggcct gccaggatcg acgacatcgc 150
ggatgggcgc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaacca aggaacctgt cccctacgac 250
aaatgtaaag acaagtaagg gaagcccaac aagaggaaaag gottcaatga 300
agggctgtgg gagatccaga acaacccccca cgcacgtac agcgccttc 350
cgccagtgcg ctctccgcac agcagggccc ccgaggccaa ccccgccgac 400
ggcagtgcg ctgacgagga cgatgaggac cgggggggtc tggccgtcac 450
agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
cagacaagag tagcgacaa cgtggcctga agaggaagac gcctgcgcga 550
aagatgtcgg ctctgaaaac agcccgaaaag gcctccagcg acctggatca 600
ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcatctgagt 650
cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
cgggcgcacc ggagggggcc tctgggggga cggaaaaaaa agaaggcgcc 750
gtcagcctcc gactccgact ccaaggccga ttcggaaggg gccaaagcctg 800
agccgggtgg catggcgcgg tggcggtcct cctctctctc ttctctctcc 850
tctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
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agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150
gagcggggca ggcgggcgag cagcggggac gacgtcaggg aggaacatga 1200

gccgcgcaag aagcgggggac gcaaggggccc gggcgggggt ccccggtcct 1250
 cctctgaact ccagcccgag gccgagctgg agagagaggg caagaaatca 1300
 gccaagaagc ccagtccttc aagcacagag ccggccagga aacctggcca 1350
 gaaggagaag agagtggggc ccgaggagaa gcaacaagcc aagcccgtag 1400
 aggtggagcg gacccggaag cggtcggagg gcttctcgat ggacaggaag 1450
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
 cagtgaagtc aagtttgccc taaaggtcga cagcccgga cgtgaagaggt 1550
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 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttgcgcgtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccgcc 1700
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 gctggccggg gaggaggccc ccagggagaa ggccggaggac aagcccgaca 1850
 ccgatctctc agcccagtg aatggcgagg ccacatcaca gaagggggag 1900
 agcccgagag acaaggagca ccaggagggt ccggactcgg aggaggggccc 1950
 aaggtgtggc tctctgaag acctgcaaga cagcgtaagg gagggtcctg 2000
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 gcccccgcc gagctcaggc tgcccctctc ctccccggc tcgcaggaga 2150
 gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttcctt 2200
 gggttttttt ttctgccta atttctgtga ttccaacca acatgaaatg 2250
 actataaacg gttttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

35										40					45				
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro					
				50					55					60					
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys					
				65					70					75					
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala					
				80					85					90					
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala					
				95					100					105					
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp					
				110					115					120					
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala					
				125					130					135					
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser					
				140					145					150					
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
				260					265					270					
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
				275					280					285					
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
				305					310					315					
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg					

320										325					330				
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Arg	Leu	Arg	Glu	Gln				
				335					340						345				
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly					
				350					355					360					
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg					
				365					370					375					
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly					
				380					385					390					
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu					
				395					400					405					
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser					
				410					415					420					
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg					
				425					430					435					
Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr					
				440					445					450					
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys					
				455					460					465					
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser					
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
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Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile			
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(210) 315
 (211) 370
 (212) PRT
 (213) Homo sapiens

(400) 315
 Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr
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 Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
 35 40 45
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150

Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
				155					160					165	
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
				170					175					180	
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
				185					190					195	
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
				200					205					210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
				215					220					225	
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
				230					235					240	
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	
				245					250					255	
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	
				260					265					270	
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	
				275					280					285	
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	
				290					295					300	
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	
				305					310					315	
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly	
				320					325					330	
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	
				335					340					345	
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
				20					25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
				35					40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
				50					55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
				65					70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
				80					85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
				95					100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
				110					115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
				125					130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
				140					145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
				155					160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
				170					175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
				185					190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
				200					205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
				215					220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
				230					235					240

Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val		
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala		
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn		
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu		
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu		
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys		
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala		
350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys		
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val		
380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser		
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr		
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro		
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln		
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro		
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala		
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys		
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp		
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro		
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val		

	530		535		540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545		550		555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560		565		570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575		580		585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590		595		600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605		610		615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620		625		630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635		640		645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650		655		660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665		670		675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680		685		690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695		700		705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710		715		720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys
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<210> 318

<211> 23

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 319

ctgtgctctt cgggtgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 320

ccacagatgt ggtactgctt ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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ttgtggastg gtgttttgta tcttggccct aactctaatt gtctgtttt 200

gggggagcaa gcacttcttg cgggaggtac ccaaaaaagc ctatgacatg 250

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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80								85				90					
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe			
				95					100					105			
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys			
				110					115					120			
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro			
				125					130					135			
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe			
				140					145					150			
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn			
				155					160					165			
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn			
				170					175					180			
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu			
				185					190					195			
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				200					205					210			
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro			
				215					220					225			
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu			
				230					235					240			
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe			
				245					250					255			
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				260					265					270			
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly			
				275					280					285			
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys			
				290					295					300			
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly			
				305					310					315			

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 gtccccggcg ggactgtcaa tggaggcagg ggttcacgca caaagtctac 900
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950
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 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttgga 1100
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20		25		30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser					
	35		40		45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly					
	50		55		60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln					
	65		70		75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu					
	80		85		90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr					
	95		100		105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu					
	110		115		120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala					
	125		130		135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro					
	140		145		150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr					
	155		160		165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu					
	170		175		180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln					
	185		190		195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala					
	200		205		210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val					
	215		220		225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val					
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<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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gcacggggc caccgggatg gacatytga gcaccaggga cctgtaagac 200

aaccccgtaa cctccgtgtt ccagtaacgaa gggctctgga ggagctgggt 250
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gtcctgggtg ccattggcct cctgggtatcc atctttgccc tgaaatgcct 400
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tccttccaag cagcactatg tgtaatgctc taagaacctc cagcacgggc 900
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atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
catctttgga gaggcctaat ggtcttagcc tcagtctctg tctctaaata 1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
ccccctcttc ctctagtcac ataaacccat tgatgatcta tttccagct 1250
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ttctgctgtt tgaattttgt ctcgccaccc ccacttggc tagtaataaa 1350
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
cccatgatct cgggtttctt acactgtgat cttaaaagtt accaaaccaa 1450
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 gactagcctg ggcaacatgg agaagcctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattcggg 1950
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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val	
				165					165					165	
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val	
				170					175					180	
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala	
				185					190					195	
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser	
				200					205					210	
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe	
				215					220					225	
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile	
				230					235					240	
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro	
				245					250					255	
Ser	Lys	His	Asp	Tyr	Val										
				260											

#210 - 327
 #211 - 2010
 #212 - DNA
 #213 - Homo sapiens

#400 - 327
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 gtgggcacag tggctgtcac tgcatgctt cagtggagag tgtcggcctt 200
 cattgaaaaa aacatcgtgg tttttgaaaa cttctgggaa ggaactgtgga 250
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 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350
 tctctcttcc gtgatgtctt tcttgcttt catgatggcc atccttgga 400
 tgaaatgcac caggtgcacg ggggacaatg agaagggtgaa ggctcacatt 450
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 cctgtgagc tgggttgcca atgcatcat cagagatttc tataactcaa 550
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 actcaactat tgccttttcag ggaaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcttc catttataat 1300
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 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
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<211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly
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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp
				20					25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
				35					40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
				50					55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
				80					85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
				110					115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
				125					130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
				140					145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
				155					160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
				170					175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
				185					190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
				200					205					210
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329

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 gctgtggat gtctgtgtg gtgcagagca cggccagat gcagtgcag 200
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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu	1	5	10	15
Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp	20	25	30	
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val	35	40	45	
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly	50	55	60	
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val	80	85	90	
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr	95	100	105	
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr	110	115	120	
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro	125	130	135	
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr	155	160	165	
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Gly	Gly	Gly	Gly	Leu	170	175	180	
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His	185	190	195	
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly	200	205	210	
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val	215	220							

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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 ggaagggctc tggatgaatt gcctccgaca agccagggtc cggttgcaat 300
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 caagtgtaca atgatggact acttattact ttttgacct catgtattat 1100
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 agaagtatcc agtgggtggc atccctgccc ccattacata cctaccagtt 200
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<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334
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 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75
 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

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 tggccctgac cgggctggcg ctgctcctgc tctgtgtgtg gggcccaggt 150
 ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200
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 tctttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
 cccgaggtgc agcagtggtc ccagcagttt ctctacatgg gctttgatga 350
 agcgaaattt gaagatgaca tcaactattg gcttaacaga gatcgaaatg 400
 gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
 gcaattggtc cccggagccc ctaaggcttt aggcattggg ccagcgtcaa 500
 ctaogatgac tactaaccat gaattgccac acgctgtaca agaagcaaat 550
 agcgattctc ttcattgata tctaattgcc ttacactact tggttttctga 600
 tttgtcttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttta aacaacacat gtaaatgcct ttgatattt catgggaatg 700

ctctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
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Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
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tgaaggggtg ggtgatgagg tgacctctt tttctgggtg cttgctgac 150
ttctgggtgt ggcccttgcc tgggtctcaa cgacacccgc tgagggcggg 200
gacctactgc ccagccgtc agggacccca accgatccc agcccagcgc 250
agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

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ccccagcct gagacacaga ggtcaagctg cacagccaga gccagccag 350
gggttcacag caacacccgc agcccgggac tcccgcagg agccctcgt 400
gctacggctg aaatttcaca atgattcaga gcaggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga ccagtttcc cggccgggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
gacctgggc agccttcacc tccctcccaa ctgcttctc cactgccaag 600
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<L10> 338

<L11> 246

<L12> PRT

<L13> Homo sapiens

<I00> 338

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  1             5             10             15

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Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
      20             25             30

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Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
      35             40             45

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Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
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Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
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Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

01100 339

01110 849

01120 DNA

01130 Homo sapiens

04000 339

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tgcctctccc agattcccca ggctctcaga gaagatcaga agaaagtctg 100

caagacccta agaaccatca gccctcagct gcaacctctc cctcccaagg 150

atgacaaaagg cgtactcact ctatttggtc agcagctttc ttgcctctaaa 200

tcaggccaga ctcatcagtc gatgtgaatt ggcacaggtg ctgcagctgg 250

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 ctgctgaata ccaacctttct tgcaggcact cactggcgaa aaaggattgt 500
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<210> 340
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 340
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 20 25 30
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
 35 40 45
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
 50 55 60
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
 65 70 75
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
 80 85 90
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
 95 100 105
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
 110 115 120
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
 125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtraggcgc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatactgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtgpatgcoo gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg cccataatca ggcagaccta atcagtcgct gtagc 45

(210) 346

(211) 2575

(212) DNA

(213) Homo sapiens

(400) 346

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actjagaacc caccagctca tccagacac ctcatacaca cctatcttata 100

caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150

aaggagaaaa cgggggtaaa gggagggag caattcaatt tgaagtccct 200

gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250

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aaatttcag gtggaacaag caaccatgt tctgtgtcaa gottgaagga 400

gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450

gttcctagcaa catgtctcta aggaagcgat acaggcacag accatgcaga 500

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aagccagcaa gcacagccct gaagccaggt accgcttga ctttggggaa 650

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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
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Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
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Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
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Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
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Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val
560 565 570

Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln
575 580 585

His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser
590 595 600

Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu
605 610 615

Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe
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Asp Gln Ile Asn Ala Val Asp Glu Arg
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<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

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<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcaactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgtg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens

<410> 351

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 tcaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5				10					15	

Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20			25						30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggttcc tggccctgc ggtgctccca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgcccctg ggagaaggcc 200
 ccgtggagag caccagcccc ggcggggagc ccgtggacac cggcccccca 250
 gccccacccg tcgcgcacag acccgaggac agcaccggcg aggagcggct 300
 ggaccagggc ggcggttcgc tggggcccg gctatctgcg gccatcgtga 350
 tcgcgcacct gctggccacc tgcgtggtgc tggcgtctgt ggtcgtcgcg 400
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 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PFT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
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 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120
 Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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 gttggccggc ggcgggccgg gacgggcctg gccctgtatc tgtgctggt 100

gtgootgaag gggggggtgg cccacgggtg totgcaatgc cacagcaact 150
tctccaagaa gttctccttc taccgcccac atgtgaaatt caagtcootgg 200
tgggtggggg acatccccgt gtcagggggg ctgctcaccg actggagoga 250
cgacacgatg aaggagctgc aactggccat ccccgccaag atcaccggg 300
agaagctgga ccaagtggcg apagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggttat tccccaaag agctgogaaa 400
catcttccgg gagcaggtgc aactcatcca gaacgccatc atcgaaaggc 450
aactggcacc aggcagctgg ggaggagggg agctctccag ggagggacc 500
agcctagcac ctgaaggatc aatgccatca ccccgggggg aactcccta 550
agtacccccc agaggcgctg ggagtgttgc caccgacctc cactgaagtt 600
tgctccatct cactctgggg gtcaacctgg ggaaccttc cctccggggc 650
atggacacac atacatgaaa accagggcgc atcgactgtc agcacogctg 700
tggcatcttc cagtaacgaga ccatctcttg caacaaactg acagactcgc 750
aactcgcctg ctttggttat aactggaggt agggctcagg catcacccc 800
accgtgcca gggccctact gtccctgggg tccagggctc tcttggagg 850
gggtcccccg ccttccactt ggtgtctatc gggtagggcg gggccgtggg 900
ttcagggcg caccacttcc aagcctgtgt cccacaggtc ctggggcgag 950
tggaagtccg ctgtccaggg cctcctgaac tacataaata actggcacaa 1000
gtaagtcccc tctcaaaac aacacaggca gtgtgtgtat gtgagcaact 1050
cgtgggtgag tatgtgtggg gcacaggctg gtcacctcag ctccacgtc 1100
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cgggcactct tctaaaagg tcccatagg gtctggttcc acccatccc 1250
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ccatggaggg gctgactgcc ccacattgcc ttccagacag gacacgagca 1350
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aaccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550
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 ggcctcggga gaaggggtgc tegttaagcca acaccagcgt gccggggcct 1650
 gcaacacctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
 cataggacca cactgccag ctgggaggag aggcctgggg ccccaggga 1750
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 gcagcctggt atcgccagcc ttaaggtgtc tggagccccc acacttggcc 1850
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
 gctgggcctg ccccaggga acgtgggggc ggagactcag ctggacagcc 1950
 cctgcctgtc actctggagc tgggtgtctg ctgcctcagg acccctctc 2000
 cgacccccga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050
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 ctgogggatg tgattaaagt cctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1 5 10 15
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln

125

130

135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro
 140 145 150

Ser Pro Arg Gly Asp Leu Pro
 155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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 ttgagaaatc ctccagatggc cctgggtgctg cccaggaacc cactggctc 150
 acagatgtcc cagctgccat ggaattcatt gctgcactg aggtggctgt 200
 cataggcttc ttccaggatt tagaaatacc agcagtgcac ataactcata 250
 gcatggctga aaaattccca ggogtgcctt ttgggatcag cactgattct 300
 gaggtttctga cacactacaa catcactggg aacaccatct gctctttctg 350
 cctggttagac aatgaacaa tgaatttaga ggacgaagac attgaaagca 400
 ttgatgcac ccaattgagc cgtttcattg agatcaacag cctccacatg 450
 gtgacagagt acaaccctgt gaotgtgatt gggttattca acagcgtaat 500
 tcagattcat ctctctctga taatgaacaa ggctcccca gagtatgaag 550
 agaacatgca cagatccag aaggcagcca agctcttcca ggggaagatt 600
 ctctttatto tgggtggacag tggatgaaa gaaaatggga aggtgatata 650
 atttttcaaa ctcaaaggagt ctcaactgcc agctttggca atttaccaga 700
 ctctagatga cgagtgggat acactgccca cagcagaagt ttccgtagag 750
 catgtgcaaa acttttctga tggattccta agtggaaaat tgttgaaaga 800
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaaact tgaattctcc 850
 ttggaactac atatggccaa gtatctaact tatgcacagt aaaaaggcac 900
 aactcaaatc tcagagacac taaacaacag gatcactagg cctgcacaac 950
 acacacacac gcacgtgcac acaogcaogc acgogtgcac acacacacgc 1000
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 tctctctctt ctctctttta atttcatac ctcaactcct atcaatttc 1100

atttattatcg tgcattcata ctctgtaagc ccattctgtaa cacacctaga 1150
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 ctagagaaag attgttcbaa tttgtcattt aatatcaagt ttgtatactg 1250
 cacatgaatt acacacaaca tagttcctgc tcttttaagg ttacctaaagg 1300
 gttgaaactc taccttcttt cataagcaca tgctcgtctc tgactcagga 1350
 tcaaaaaacca aaggatggtt ttaaaccact ttgtgaaatt gtctttttgc 1400
 cagaagttaa aggtctgtct caagtccctg aactcagcag aaatagacca 1450
 tgtgaaaact ccattgcttg ttatcatctc caactcccta tgtaaataca 1500
 caacctgcatt aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
1				5				10					15	
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
			20					25					30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
			35					40					45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
			50					55					60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
			65					70					75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
			80					85					90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
			95					100					105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
			110					115					120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
			125					130					135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
			140					145					150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
			155					160					165	

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

ccagcagtgcc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tgagagtggtg gatacactgc 20

<210> 361

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

ggtctataggga aattctctgct gtgg 24

<210> 362
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<410> 362
tattccagggc gtgtcatttg ggatcagcac tgattctga; gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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ccggcgccggg tggcgagag atcagaagcc tcttcccaa gccgagccaa 100
cctcagccggg gacccgggct cagggacgcg gcggcgccgg ccgcgaactg 150
agtggctgga ccatggcagc gtccgcggga gccggggcgg tgattgcagc 200
cccagacagc ccggctgagg tctggctggg gctggcgccg gcgcttgagg 250
tcttgacagc tggagtatca gccttggaag tatatacgc aaaagaaatc 300
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tagtaagact ggcgggctga cctcagcttc ctggagcttc cagccagagg 400
gggcgcacac taatgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcacaa tcaacataga aaatatgcag tttatacaca 550
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tcagtttgg gtagtggcgg gcatagttac tgcctgggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaaacgggatt acaatggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct ccgaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900
tccggcgga acacagtgca caagattaac aagtcagagt ctgtggtgta 950
tgccgatata ccgaagaatt aagagaata ctagaatata tctccagcaa 1000

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 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattc agaaatgggt 1300
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 cagtatcagt accattttatt tgtctgcgcg ttttaaaaaa taccattgg 1500
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 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggttttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
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 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	
				95					100					105	
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	
				110					115					120	
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	
				125					130					135	
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	
				140					145					150	
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	
				155					160					165	
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	
				170					175					180	
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	
				185					190					195	
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	
				200					205					210	
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	
				215					220					225	
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	
				230					235					240	
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	
				245					250					255	
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		
				260					265						

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
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 ccataagcgc gccgggctgc cgcctctcgg ccacggctgg gtccgggggc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 agggggcggg cccggggcga gtcccccgcg gcccccagacc ctgaggcgtc 250
 gcctctggcc gagccgcac agggagcagtc cctgcgcccg tggctctcgc 300
 agaccccggc gccgcctgc tccaggtgtc tcgcacagag cctcagagag 350
 agccgggacc tgtgcacag gatcaaggat gagggtgggg caccggggcat 400

agtgggttggga gtttctgttag atggaaaaga agtctgggtca gaagggttag 450
 gttatgctga tgttgagaa cgtgtaccat gtaaacacaga gacagttatg 500
 cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgcacaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgcacaaca 650
 agattactga ttcccatctt aagtggcaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgcgggaa 850
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccttaagatt atttaaaaaat 950
 gactctttgt tcttcaaac ttgttagtcag tttttgtatt caacttttgg 1000
 ctataacctc ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050
 tggactatat gcagaaaata ttccatgaat tggatatgt gacgaactgt 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
 ctctctgtgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
 aagtcacaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

*210 - 366
 *211 - 373
 *212 - PRT
 *213 - Homo sapiens

*400 - 366
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1 5 10 15
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367
<211> 31
<212> DNA
<213> Artificial Sequence

<210>
<213> Synthetic oligonucleotide probe

<400> 367
tggaagagaa gtctggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial Sequence

<210>
<213> Synthetic oligonucleotide probe

<400> 368
catttggtt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial Sequence

<210>
<213> Synthetic oligonucleotide probe

<400> 369
aaaactcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial Sequence

<210>
<213> Synthetic oligonucleotide probe

<400> 370
gtctacacat gggtgtctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgaactat agaagagta tgaagtgca tgaagtgta cgttaagctg 50

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu		35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe		50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu		65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu		80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn		95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp		110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys		125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val		140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro		155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu		170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly		185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala		200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys		215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser		230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly		245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu			260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgcgtgc tggaaacccga gccggagccg gagccacagc ggggaggggtg 50

ggtggggcgc ctatggggg aggtgtccg ggtgtccg ccagacggggg 100

cagcaggtcg tccggggggc caccatgctg gtgaactgct acccttgctt 150
tgttaggcctc ctggcctcct gctggggct ggaactgtca agatgcgggg 200
ctaaaccccc tgggaagggc tgcagcaatc cctccttctc tgggtttcaa 250
ctggaacttct atcaggtcta ctctctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctctttctc ctgaacttact cactatgctg cttaacccaa ctctctcaag 500
actaatttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggctgggtat atccatgagc acgtggaacg 600
gcctgaactc cctgctgagt ggatcccagc tacctttgct cgagctgct 650
cttggaacca tgtgtggct gtagtggcag gtgtggcagc tgaggctgta 700
gcagctgga tagggctggg gctgtagcg ccttttgtgg ctgcctccc 750
tctctggct ctggcagggg ccttggcctc tggaaactgg ggggagaact 800
atgacggga gctgctctc tcaaggacct gtgtggagg cctgcctgct 850
ctctgtcgg accgcgcgt gctgctgctg ggcaccatac aa jctctatt 900
tgagagtgtc atcttctct ttgtcttct ctggacact gt-gctggacc 950
cacaggggc cctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggt ctctcctgta ccgtatcgcc acctccaga ggtaccact 1050
tcagcccatg caactgctgt ccttgcctgt gctcctgct gtctctctc 1100
cttctatgtt gaattctct accagcccag gccaggagag tccggtggag 1150
ctctctatag cctttctact tattgagttg gcttgtggat tatactttc 1200
cagcatgagc ttctacgga gaaaggtgat cctgagaca ggcaggtg 1250
gtgtaactca ctggttccgg gtaactctgc actcactgga ttgcctaggg 1300
ctccttgctc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tgggtgatgc tctgctgga gtggtgggac 1400
cttccacgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagcct atgcctctga gctgtaacc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgaacttt gtgaactgtcc tgtgggtttct cctggcattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaaggtag caaaagtcc 1650
 ctctgtgtta ctcccattta gaaaataaac acttttaaat gatcaaaaaa 1700
 aaaaaa 1706

<210> 374
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 374
 Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
 1 5 10 15
 Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
 20 25 30
 Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
 35 40 45
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
 50 55 60
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
 65 70 75
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
 80 85 90
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
 95 100 105
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
 110 115 120
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
 125 130 135
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
 140 145 150
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
 155 160 165
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
 170 175 180
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
 185 190 195
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
 200 205 210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gggggggggc gagaggaaac ggggggcggg gccgggcccg 50

ggcctggaga tgggtcccgg cggcgggggg tgggtgttgc togtgatctg 100
 gttccccggg tgggtggggg cccacgggct cggtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatcaccttt cacagccaca 200
 cctggccaagg actttgggtg tatctttcac acaagggtatg agcagattca 250
 ccttgtcccc gctgaacctc cagaggcctg cgggggaactc agcaacgggt 300
 tcttcattca ggaccagatt gctctgggtg agaggggggg ctgtccttc 350
 ctctccaaga ctgggtgggt ccaggagcac ggcgggcggg cggtgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaacca ggcacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccggcg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600
 tgcaacggcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgaat ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttggggggt gctaggtctg aagggaagcc acaccactgg ccttccttc 800
 cccagggccc ccaaggggtg ctcatgctac aagaagaggg aagagacagg 850
 ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcttgagage catctgtgac ctgtcacact caactggctc cagcctcccc 950
 taaccagggg ctctgcacag tgaccttcac agcagtttgt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taagcttct catcaggggt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

210 376

211 188

212 PRT

213 Homo sapiens

400 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10					15	

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25					30	

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Gln	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Gln	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln		
				95				100					105		
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377
 <211> 496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 actgactcca ctgctctgtg ctgggacat ggaacttgca ctgctgtgtg 50
 gggtgggtgt gatggctggg gtgattccaa tccagggggg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgcca tcctctccta 150
 ctggccttac ggtctgtact gggactagg tggcagaggg caaccacaag 200
 atgcaacgga ctggtgtgtc cagacccatg actgtgtgta tgaccactg 250
 aagaccagg ggtggggcat ctacaaggac aacaacaaaa gcagcatata 300
 ttgtatggat ttatctaac gatattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

<210> 378
<211> 116
<212> PRT
<213> Homo sapiens

<400> 378
Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15
Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30
Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45
Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60
Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75
Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90
His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105
Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 379
ctgactccac tgcctctgtgc tggg 24

<210> 380
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 380
cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
<212> DNA
<213> Artificial Sequence

<221>
<223> Synthetic oligonucleotide probe

<400> 381
ctgaataaga tggtaagca agtgactggg aaaatgcca tcttc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50
ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100
gcccgggat gcacgggcca gaggccatgc tgctgctgct cagcttggc 150
ctctggggg gcccacactg ggcagggaag atgtatggc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccattgaaatc acagggtctc 250
gggtgtctgt aggtcttctc ctgggtgaaaa gtgtccaggt gaaaacttga 300
gaactctggg aagtgaact gggagcctta ggtgggaata cccagggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
cttctctcgg gggtatggtc atgtacacca gcaaggaccc ctatttctat 450
tttgggaagc ttgatggcca gatctctctt gctacccca gccaaagagg 500
gcagtgctg gtgggcctct atggccagta tcaactcctt ggcattcaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaate tcacatactc agcaaaactca cccgtgggtc gctagggtyg 650
ggtatggggc catccagact gaggccatct gtgtgggtgg ggctgatggt 700
acttgagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly	20	25	30
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr	35	40	45
Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln	50	55	60
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly	65	70	75
Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr	80	85	90
Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met	95	100	105
Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly	110	115	120
Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val	125	130	135
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly	140	145	150
Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro	155	160	165
Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg	170	175	

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
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 agctctgtgg ctgaactggg tgcctcatcac gggaactgct gggtatgga 100
 atacagatgt ggcagctcag gtagccccc aaattgctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaacgcg 200
 cccctcccca ccccccacaaa aaactgtaaa gatgcacaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgcg gogaatggcg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaagaata 350
 atgttccaaa atcgggtccat ctcccaaggg gtcccaatttt tottctggg 400
 tctcagcagc ccctgactca ctacagtcca gatgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc ttggaacaat 500
acaaaggatg ggtttcaatg taattagget actgagggga tcagctgtag 550
caatgggtat agccccact gtcttactga caatgctttt ttctggcgaa 600
cgaggatgac ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tatatctget ggttgcttag 700
gtttgtccct tegtataac agcttcaaa aacttaagta taatcaattt 750
aaagggtcca accagctcac ctggtatatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tctattttt ttaacaatac cttcagacct 900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
gggtataact cctgagaacc atccctgtgc gaatattcca agactgcgcg 1050
aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
cagaaccttt acttgacgtg gaataaaatc agtgtcatag gacagaccat 1250
gtctgggacc tggagctcct tacaaggct tgatttatca ggcaatgaga 1300
tcgaagcttt cagtggacc agtggttttc agtgtgtccc gaatctgcag 1350
cgctcaaac tggattccaa caagctcaca tttattggtc aagagatttt 1400
ggattcttgg atatccctca atgacatcag tottgctggg aatatatggg 1450
aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
ggtctaaggg agaatacaat tatctgtgac agtcccaaag agctgcaagg 1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
cccaagctcc ccaggccgaa gcattgagag aaacccccct tgcctccgac 1700
ggtgggagcc acagagcccg gccagagac cgatgctgac gccagacaca 1750
ctcttttcca taaaatcacc gggggcagcg tggcgctttt cctgtccgtg 1800
ctcgtcctcc tctgtgttat ctaagtgtca tgggaagggt accctgcag 1850
catgaagcag ctgagcagc gctcctcat gggagggat aaggaaaaaa 1900

aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
 gattataaac ccaccaaac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
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 tcataatact ggtcattttc ctctcataca taatcaacc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
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 aaaacttctt tcataggtaa aaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
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 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150

Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	
				155					160					165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	
				170					175					180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	
				185					190					195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	
				200					205					210	
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	
				215					220					225	
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	
				230					235					240	
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	
				245					250					255	
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	
				260					265					270	
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	
				275					280					285	
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	
				290					295					300	
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	
				305					310					315	
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	
				320					325					330	
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	
				335					340					345	
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	
				350					355					360	
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	
				365					370					375	
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	
				380					385					390	
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	
				395					400					405	
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	
				410					415					420	
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	
				425					430					435	

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
 440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
 455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
 470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
 485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctcgcgatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggtccctagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctcagtttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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ggatcttcaa cgatagggat ctgtgttttg ccgtattcc agttgggtgt 150
ctcggaccta ccattgogaag aagatgaaat gtgtgtaaat tataatgacc 200
aacacctcaa tggctggtat atctggatcc tctgtgtgt ggttttggtg 250
gaagctcttc tctgtggaga tgtggtcttc tgcctccagt gctggctgag 300
gagacccoga attgattctc acaggcgacc catggcagtt tttgtgttg 350
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaaactca aacctgtgac ctatctctg ttctgtctcc 450
atgttttggc cctttaggct ccccaacctc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgttg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaat taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
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gtagtttcca ccacatttag gactccactg cagtatacag cacaccattt 850
tctgctttta actctttcct agcatgggt ccataaaaaat tattataatt 900
taacaatagc ccaagccgag aatccaaat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gaggaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100
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cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagt gcattttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tcttcaaaa aacaataaac atcaatgat atctaaaaa 1449

<210> 390
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 390
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 20 25 30
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
 35 40 45
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
 50 55 60
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
 65 70 75
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
 80 85 90
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
 95 100 105
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
 110 115 120
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
 125 130 135
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
 140 145

<210> 391
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 391
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<210> 392
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 392

ccaaaaatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccatttggtg ctctcggacc taccatgga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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aagctccgtg gggcgggaga ccgtgacgag aagcccacgg ccagctcagt 200
ctctctctac ttggggagag agagaaagtc agatgcctct tttaaactcc 250
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ttttcaagtc ttgatttggt gttacctca agttaccatt ttccagtcac 400
gtctgtttgt ttgcttcttc agaaatgttt ttacaaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttctt tgtatttgga ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaaagcagt 550
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aagotctaca cactttccaag gactatgctg gattcatgga actctaattc 1000
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<211> 140
 <212> PRT
 <213> Homo sapiens

<400> 395

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Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20				25						30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35				40						45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50				55						60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65				70						75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80				85						90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95				100						105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110				115						120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125				130						135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396

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<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
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 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe	Ser
95	100		105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly	Leu
110	115		120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser	Asp
125	130		135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser	Ala
140	145		150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp	Leu Ser
155	160		165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
170	175		180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
185	190		195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
200	205		210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
215	220		225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
230	235		240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
245	250		255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
260	265		270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
275	280		285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
290	295		300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
305	310		315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
320	325		330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
335	340		345
Ala Ala Arg Gly	Pro Thr Ile Leu		
	350		

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

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<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggtaggtgcc cgaaaggtec agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttaaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gaggctatat gogtcaatto cccaaaacaa gttttgacat ttccctgaa 150

atgtcattct ctatctatct actgcaagtg cctgctgttc caggccttac 200

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cgactgtgac caccaaactg cactcagact ctgaactcag acctgaaato 300

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tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

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aaatcttaag gaggactgag tctttgcaag acacaaaagcc tgggaatcga 600
 tggctgctcc tgggcacattt gctaagactc tatctggaca gggatatttaa 650
 aaactaccag accctcgacc attatactct ccggaagatc agcagcctcg 700
 caatttcctt tcttaccatc aagaaggacc tcgggtcttc tcctgcccac 750
 atgacatgcc attgtggjga ggaaaccaatg aagaaataca gccagattct 800
 gactcacttt gaaaagctgg aacctcaggc agcagttgtg aaggcttttg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt 1000
 ctgtgctggg tcacagtgtc tcttatttat gcattacttg ctctcttgca 1050
 tgattgtctt tatgcacccc caatcttaat tgagaccata ctgtataag 1100
 atttttgtaa tatctttctg ctattggata tatttattag ttaatatatt 1150
 tatttatctt ttgtattta atgtatttat tttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctagggggggt tcttcatttg ttttcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccaccccag tagactccc agtcccataa ttgtgtatct tccagcccag 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25				30		
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40				45		

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85					90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
				95					100					105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
				110					115					120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
				125					130					135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
				140					145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
				155					160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
				170					175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
				185					190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
				200					205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
				215					220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
				230					235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
				245					250					255
Trp	Met	Glu	Glu	Thr	Glu									
				260										

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgttgtt ctccagattt caggcata 28

<210> 404
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
agtcctcctt aagattctta tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggcttttgc cgtgaccca gagatggccc cgagcgagca aattcctact 100
gtccgggtgc ggggtacccg tggcgagct agcaaccttt cccctggatc 150
tcacaaaaac tgaactccaa atgcaaggag aagcagctct tgcctgggtg 200
ggagacgggtg caagagaatc tgcacctat aggggaatgg tgcgcacagc 250
cctagggtac attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgcct ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcacctttgg aaatcagtcg ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaaat gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcctag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650
accacttatg atacagtga acaactactg gtattgaata caccacttga 700
ggacaatata atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttcctattct gggaacacca gcgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aagggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttgggtg agaatgaccc cttgggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcactc ctttttaa 998

<210> 406
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
1				5					10					15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr		
	260	270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly		
	275	285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met		
	290	300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg		
	305	315
Glu Met Ser Gly Val Ser Pro Phe		
	320	

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgaggatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ggggaattct taaaatggac tgactccact cacc 34

<210> 409

<211> 1437

<212> DNA

<213> Homo sapiens

<400> 409

gggacgggtg ggcgcgggac gcgggcaggg ttgtggcgca gcagtctcct 50

tcctggcggc ggcctgaag tcggcggtgg cgtttgagga agctgggata 100

cagcatttaa tgaaaaatct atgcttaaga agtaaaaatg gcaggcttcc 150

tagataatct tcgttgccca gaatgtgaat gtattgactg gactgagaga 200

agaaatgctg tggcatctgt tgtgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tccaaagcca gaacagttga 300

accatgcctt ccacacatgt ggtgtatttt ccacattggc ttctctcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
 ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450
 tgatgtttgg gtcacttatt gcttccatgt ggatttcttt tgggtcatat 500
 gttacccaaa ataactgatgt ttatccggga ctagctgtgt tttttcaaaa 550
 tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttctt ttgtttatat 650
 tctgtttgta gatagggttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcatggcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcttgag atttagaact tgatctactc cctgagccag ggttacatca 900
 tcttgctatt ttagaagtaa ccactcttgt ctctctggct gggcacgggtg 950
 gctcatgctt gtaatcccag cacttttgga ggccgaggcg ggccgattgc 1000
 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgcagt gagctgagtt tgcgcactg cactctagcc tgggggagaa 1200
 agtgaaaact cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 caagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaagggt tttcagcaag ttgttaacta ttttggcta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcocaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttctctaat atgaacttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20				25					30	

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<210>
 <223> Synthetic oligonucleotide probe

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<210>
 <223> Synthetic oligonucleotide probe

<400> 412
 ccagaaactoga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<210>
 <223> Synthetic oligonucleotide probe

<410> 413

atggcaggct tcttagataa tttctgttgg ccagaatgtg 40

<211> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<410> 414

gttgatggca aatttcttca aaggaggggg agagctgtgg cagggcagga 50

gcagctggcc cactgggggc ccgcaacaact ccgtctcacc ctctggggccc 100

actgcattca gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtgggtggc agctgggtca 200

gggacctacg gcacctgtgt gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtgggaag ctgaccccaa gccaccttc 300

acctggacag gatgagagtg tcaggtgtgc ttcgctctct ggccctcacc 350

tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaaac atccgtctgc cactgtggct ggcagccctg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcattcaagg ctgcccagcc 500

aactactttg cgttttaaat ctgcagtggg gcgcaccaag tcgtggggcc 550

tactatgtgc ttggaagacc gcattgatcat gactctgtg aaaaaacaatg 600

tgggcagagg cctaaacatc gccctgggtga atggaaccac gggagctgtg 650

ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaatct cgggggggtgc actggtgtgt gtggccctct 750

acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800

gaattgggga gttctctacc aaaacaactg ggcttcgggg acagctgggt 850

cttcatagga gccaaagacc tcaggggtaa aagcccttt gagcagttct 900

taaagaacag ccacagacac aacaaatacg agggatggcc agagctgtgt 950

gagatggagg gctgcattgc ccgaagcca ttttaggggt gctgtgggtc 1000

ttctcagcc aggggcctga agaagctctt gctgactta ggagtcagag 1050

ccggccaggg gctgaggagg aggagcaggg ggtgctgctt ggaagggtgt 1100

gcaggtcctt gcacgtgtgt tcgcgcctct cctctctgga aacagaaccc 1150

tcccacaga catctaccc ggaagaccag cctcagagg tccttctgga 1200

accagctgtc tctggagaga atgggtgtgt ttcttcaggg actgctgacg 1250
 gctggctcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
 tatttttgcgt ggttttgaaa aaaaaaaaaa aaaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
ggcatatca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
tgtgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
attctctcca cagacagctg gttc 24

<210> 421

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
gtacaagtgt ggcttcacca agccctgccc agccaactac ttggcg 46

<210> 421
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1529
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgttcctgggg atccagaaaac ccattgatacc ctactgaaca ccgaatcccc 100
tggaaagccc cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgcacgga gctcgtctgc totctctctc totctctcac tcttcctctc 200
ctctctctct gcttgctcta gtctctctagt cctcaaatc ccagtccct 250
gcaccccttc ctgggacaat atgttgctct ccgcctctct gctggaggtg 300
atttggtacc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggctcag gaccattggc cagcctctta cctgagtggt ggaaacaatg 400
cccagtctcc catgatatt cagacagaca gtgtgacatt tgacctgat 450
ttgcctgctc tgcagcccc cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtcca actctctctg cctctaccc 550
tgttatctggg tggacttccc cgaatatatg tagctgccc gctccacctg 600
cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
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atgacagctt gactgaggt gctgagagga ctccagggct ggctgtctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
cttgagtcac ttgatgaag tcaggcataa agatcagaag acctcagtgc 850
ctcccttcaa cctaagagag ctgctcccca aacagctgg gtagtacttc 900

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 cagaactacc gagcccttca gctctcaat cagcgcctgg tctttgcttc 1100
 tttcattcaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgtaggaat cttgggttggc tgtctctgcc ttctcttggc tgtttatttc 1200
 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
 catggatgtg gatgaattcc cttcatgcct atcaggaagc ctctaaaatg 1350
 ggggtgtaga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
 ccttccccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
 gaaatcctg tgttggtaat gcagagacca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgggg gatctctcct taggataaag agttgctggt 1650
 gaagttgtat attttggatc aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1 5 10 15
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Glr.
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu
 80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100 105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly
110	115 120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His	
125	130 135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala	
140	145 150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu	
155	160 165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His	
170	175 180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro	
185	190 195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe	
200	205 210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val	
215	220 225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln	
230	235 240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro	
245	250 255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn	
260	265 270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr	
275	280 285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly	
290	295 300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile	
305	310 315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser	
320	325 330
Ala Gln Ala Thr Thr Glu Ala	
335	

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 424
gtaaagtgcg tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
cagaaaacca tgatacccta ctgaacaccc aatccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aatttttcac cagagtaaac ttgagaaaac aactggacct tgagtattgt 50
acattttgcc tegtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tgggtcatta ccacagctca 150
aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc ttcccttctt taagtctgat 250
accattaaca cagatgctca cactgggggc agatctgcat ctgttaaata 300

atgctgcagg aatgacacct ggtaccacga cccacccatt gacctggga 350
 gggttgaatg tacaacagca atgcaccca catgtgttac caatttttgt 400
 cacacaactt ggagcccagg gcaatatact aagctcagag gaattgccc 450
 aaatottcac gagctcact atccattctt tgttccggg aggcattctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttc 550
 agcaggagga gcaggtgtaa atctgccc acagggaacc ccaggaggcc 600
 gctcccaac tcccagtggc acagatgacg actttgcagt gaccacctt 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
 agcaaattgga attcagtaag ctgtttcaaa tttttcaac taagctgct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatatcc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgctt ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5					10					15

Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30

Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45

Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50					55					60

Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65					70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90

Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

98	100	105
Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
110	115	120
Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly		
125	130	135
Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp		
140	145	150
Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln		
155	160	165
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp		
170	175	180
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His		
185	190	195
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln		
200	205	

(210) 430
 (211) 1257
 (212) DNA
 (213) Homo Sapien

(400) 430
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 cggagcgcggg cggagccaga cgcgcaccac gttcctctcc tcgggtctct 100
 ccgcctccag ctccggcgctg ccgggcagcc gggagccatg cgaacccagg 150
 gcccgcgcgc ctcccgcag cggctccggg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgcgcgc gagcgccctc gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatgggaatgt 300
 gattacaagg gccagcagga gtgcctggtc gagaaggag cctgggggpc 350
 aatgttatto cgggtacacc tgggatccca ggtcgggatg gattcaaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtc tggacacca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgagg agtgtacatt tacaaagatg cgttcaaata gtgtctaaag 550
 agttttgttc agtggctcac ttgggtataa atgcagaaat gcatgctgtc 600
 agcgttggtt ttccacattc aatggagctg aatgttcagg acctcttccc 650
 attgaagcta taatttattt gacccaagga agcctgaaa tgaattcaac 700

aattaatatt catggcaatt cttctgtgga aggaatttgt gaaggaattg 750
 gtgctggatt agtggatggt gctatctggg ttggcaattg ttcagattac 800
 ccaaaaaggag atgottctac tggatggaat tcagtttctc gcacattat 850
 tgaagaacta ccaaaaataaa tgccttaatt ttcatttgtt acctcttttt 900
 ttattatgco ttggaatggt tcaacttaaat gacattttaa ataagtttat 950
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gacaaaagtg 1000
 tgatttcaca ctgttttttaa atctagcatt attcattttg cttcaatcaa 1050
 aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
 acattctctc aacctataat ttggaatatt gttgtggctc ttgttttttt 1150
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
 aatttgtaaa tgttaagaat tttttttata tctgttaaat aaaaattatt 1250
 tccaaca 1257

<210> 431
 <211> 243
 <212> PRT
 <213> Homo Sapien

<400> 431
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<200>
 <213> Synthetic oligonucleotide probe

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<200>
 <213> Synthetic oligonucleotide probe

<400> 433
 agcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<200>
 <213> Synthetic oligonucleotide probe

<400> 434
 atgaggetog tacaaggcca c 21

<210> 435
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 435
ccaccctgta ccaccatgt 19

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
actccaggca ccattctgtt tccc 24

<210> 437
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
aagggtctggc attcaagtc 19

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
tgacctggca aaggaagaa 19

<210> 439
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
cagccaccct ccagtcacag g 21

<210> 440
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gaggaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tctcccatca cttccoctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
agortacaat ctctccagga aaccag 26

<210> 446
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<400> 446
caattctgga tgaggtgga ga 22

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
caggactgag cgcttggtta 20

<210> 448
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<220>
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<400> 448
caagagcgcca agtacggac c 21

<210> 449
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<220>
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<400> 449
ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccctagctga cccttca 18

<210> 451

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451

tctgacaagc agttttctga atc 23

<210> 452

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 452

ctctccct cccttttct ttgtt 26

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 453

ctctgtgcc cacagtga 18

<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 454

ccatgctgc tcagccaaga a 21

<210> 455

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 455
caggaatct ggaaacctac agt 23

<210> 456
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 456
ccctgaaaag gaaccagttt 20

<210> 457
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 457
atgagtagca cctgctgttc cc 22

<210> 458
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 458
tagcaactgc ccttggtta 18

<210> 459
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 459
aacagcaggt gcgactcctc ta 22

<210> 460
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 460
tgctaggaga cgacaccag acc 23

<210> 461
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
tggacacgtg gcagtga 18

<210> 462
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
tcacggcttc gtccattc 19

<210> 463
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 463
caccatttgt ttcttgtct ccccatc 27

<210> 464
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 464
ccggcaccct tggagtag 18

<210> 465
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 465
tcaccattag cacaggagta 20

<210> 466

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 466
agxtctttga ctgtctgtgt ggt 23

<210> 467
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 467
ggcagagatc ccacttgt 18

<210> 468
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 468
actgtctcgc ctactacga 19

<210> 469
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 469
aggtatcttc gccgtctca 20

<210> 470
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 470
aaagtccaagg tgagtccat 19

<210> 471
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtggtgty cgaaacotaa 20

<210> 472

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagctc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

aaaggccaagg tgagtcacat 19

<210> 474

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

octactgagg agccctatgc 20

<210> 475

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

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<400> 475

tcaggtgga ccccaattca gg 22

<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 476

gggaggotta taggoccaat ctgg 24

<210> 477

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

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-1-